

OM protein - protein search, using sw model

Run on: July 26, 2004, 12:38:32 ; Search time 49.3333 Seconds
(without alignments)
3991.938 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	3653	100.0	697	3	AAY88430	Aay88430 Human APP
2	3653	100.0	697	4	AAU07210	Aau07210 Human bet
3	3653	100.0	697	4	AAE10637	Aae10637 Human amy
4	3653	100.0	697	4	AAE06867	Aae06867 Human amy
5	3653	100.0	697	4	AAE02589	Aae02589 Human amy
6	3653	100.0	697	4	AAU06611	Aau06611 Human Amy
7	3653	100.0	697	5	ABB78598	Abb78598 Human APP
8	3646	99.8	697	3	AAY88428	Aay88428 Human APP
9	3646	99.8	697	4	AAU07208	Aau07208 Human bet

10	3646	99.8	697	4	AAE10635	Aae10635	Human	amy
11	3646	99.8	697	4	AAE06865	Aae06865	Human	amy
12	3646	99.8	697	4	AAE02587	Aae02587	Human	amy
13	3646	99.8	697	4	AAU06609	Aau06609	Human	Amy
14	3646	99.8	697	5	ABB78596	Abb78596	Human	APP
15	3643	99.7	695	2	AAW19484	Aaw19484	APP695	mu
16	3643	99.7	695	2	AAW19498	Aaw19498	APP695	mu
17	3643	99.7	695	3	AAW88436	Aay88436	Human	APP
18	3643	99.7	695	4	AAU07207	Aau07207	Human	bet
19	3643	99.7	695	4	AAE10634	Aae10634	Human	amy
20	3643	99.7	695	4	AAE06864	Aae06864	Human	amy
21	3643	99.7	695	4	AAE02586	Aae02586	Human	amy
22	3643	99.7	695	4	AAU06608	Aau06608	Human	Amy
23	3643	99.7	695	5	ABB78595	Abb78595	Human	APP
24	3641	99.7	740	7	ADB87314	Adb87314	Human	amy
25	3641	99.7	740	7	ADB87312	Adb87312	Human	amy
26	3638	99.6	697	3	AAW88429	Aay88429	Human	APP
27	3638	99.6	697	4	AAU07209	Aau07209	Human	bet
28	3638	99.6	697	4	AAE10636	Aae10636	Human	amy
29	3638	99.6	697	4	AAE06866	Aae06866	Human	amy
30	3638	99.6	697	4	AAE02588	Aae02588	Human	amy
31	3638	99.6	697	4	AAU06610	Aau06610	Human	Amy
32	3638	99.6	697	5	ABB78597	Abb78597	Human	APP
33	3636	99.5	695	1	AAP81692	Aap81692	Sequence	
34	3636	99.5	695	2	AAR26338	Aar26338	APP695.	3
35	3636	99.5	695	2	AAW19481	Aaw19481	APP695	mu
36	3636	99.5	695	2	AAW20233	Aay20233	Human	bet
37	3636	99.5	695	2	AAW07221	Aay07221	Amyloid	p
38	3636	99.5	695	3	AAW88434	Aay88434	Human	APP
39	3636	99.5	695	3	AAW44705	Aay44705	Human	bet
40	3636	99.5	695	4	AAE10632	Aae10632	Human	wil
41	3636	99.5	695	4	AAE06862	Aae06862	Human	wil
42	3636	99.5	695	4	AAE02584	Aae02584	Human	amy
43	3636	99.5	695	4	AAU06606	Aau06606	Human	Amy
44	3636	99.5	695	5	ABB78593	Abb78593	Human	APP
45	3636	99.5	695	5	AAG68315	Aag68315	Human	amy

ALIGNMENTS

RESULT 1

AAW88430

ID AAW88430 standard; protein; 697 AA.

XX

AC AAW88430;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human APP695-VF-KK amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15667.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Claim 133; Page 148-153; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease
XX
SQ Sequence 697 AA;

Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL VFFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKL VFFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 2

AAU07210

ID AAU07210 standard; protein; 697 AA.

XX

AC AAU07210;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP695-VF-KK.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP695-VF-KK.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild type Val substituted by Phe"

XX

PN WO200149097-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB000797.
 XX
 PR 09-MAY-2001; 2001WO-IB000797.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-502548/55.
 DR N-PSDB; AAS11710.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 XX
 PS Example 8; Page 150-152; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing an
 CC APP cleavage site recognisable by a mammalian beta-secretase, and further
 CC comprising two lysine residues at the carboxyl terminus of the amino acid
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used
 CC for assaying for modulators of beta-secretase activity; identifying
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl
 CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
 CC Agents identified by the above methods are useful for treating
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta
 CC (Abeta) peptide production, for use in designing therapeutics for the
 CC treatment or prevention of Alzheimer's disease. Probes and primers
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The
 CC present sequence represents the amino acid sequence of human amyloid
 CC protein precursor, APP695-VF-KK, used in the method of the invention
 XX
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 4; Length 697;
 Best Local Similarity 100.0%; Pred. No. 9e-254;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 3

AAE10637

ID AAE10637 standard; protein; 697 AA.

XX

AC AAE10637;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW APP695-VF-KK; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild-type Val substituted with Phe"
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17873.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Example 8; Page 120-122; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence is
CC obtained by the addition of two lysine residues (KK motif) at the C-
CC terminus of App695-VF isoform which is generated by the London mutation
CC in APP695, where Val at position 642 is replaced with Phe. APP695-VF-KK
CC isoform is useful for assaying the beta-secretase activity of human
CC aspartyl protease 2a (hu-Asp2a) protein
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 9e-254;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMP SLTETKTTVELLPVNGEFSL 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMP SLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 4
AAE06867
ID AAE06867 standard; protein; 697 AA.

XX
 AC AAE06867;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
 XX
 KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;
 KW mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 642
 FT /note= "Wild type Val substituted with Phe"
 XX
 PN WO200150829-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB000799.
 XX
 PR 09-MAY-2001; 2001WO-IB000799.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-483072/52.
 DR N-PSDB; AAD13029.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 XX
 PS Example 8; Page 150-152; 185pp; English.
 XX
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.
 CC Human aspartyl proteases can act as beta-secretase proteases useful for
 CC treating Alzheimer's disease. APP isoforms are useful for identifying
 CC modulators of amyloid-beta peptide production, for use in designing
 CC therapeutics for the treatment and prevention of Alzheimer's disease,
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
 CC and neuronal loss. APP isoforms are also used in methods for identifying
 CC inhibitors and modulators of human Asp2 activity. The invention relates
 CC to a method for identifying agents that modulate the activity of human
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used

as a means to screen in cellular assays for the inhibitors of beta- and gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in polymerase chain reactions (PCR). The probes are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence is modified human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is obtained by addition of two Lys residues (KK motif) at the C-terminal end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F mutation in APP695 isoform, where Val at position 642 is replaced with Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase activity of human aspartyl protease 2a (Hu-Asp2a) protein

Sequence 697 AA;

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
 |||
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
 Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697
 |||
 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697

RESULT 5

AAE02589

ID AAE02589 standard; protein; 697 AA.

XX

AC AAE02589;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).

XX

KW Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;

KW APP695-VF-KK; Alzheimer's disease; antialzheimer's.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

DR N-PSDB; AAD06747.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 8; Page 149-151; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This
 CC sequence is characterised by a V to F alteration at position 642 and
 CC contains two carboxy-terminal lysine residues

XX

SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 4; Length 697;

Best Local Similarity 100.0%; Pred. No. 9e-254;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660

Qy    661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
      ||||||||||||||||||||||||||||||||||||||||||||
Db    661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
```

RESULT 6

AAU06611

ID AAU06611 standard; protein; 697 AA.

XX

AC AAU06611;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human Amyloid precursor protein mutant, APP695-VF-KK.

XX

KW Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild-type Val substituted by Phe"

FT Misc-difference 696. .697

FT /note= "2 Extra Lys residues added compared to wild-type

FT APP695"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

DR N-PSDB; AAS11525.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Example 8; Page 150-152; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the

CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is the human APP695 mutant, APP695-
CC VF-KK which has 2 extra Lys residues added at the C-terminis compared to
CC APP695-VF (the London mutation). The mutation alters the specificity of
CC the APP gamma-secretase activity and increases the rate of processing of
CC the amyloid Abeta peptide

SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 4; Length 697;

Best Local Similarity 100.0%; Pred. No. 9e-254;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVONGKWDS DPSG TK 60

QY 61 TCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db 61 TCIDTKEGILOYCOEVYPELOITNVVEANOPVTIONWCKRGRKOCKTHPHFVIPIYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db 121 EFVSDALLVPDKCKFLHOEBMDVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKEB 180

QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db 181 GVEFYCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE 240

Qy 241 EADDEDEDEDGDEVEEEAEEPYYEATERTTTSIATTTTTTTTSEVEEVVRVPTTAASTPDAV 300

Db 241 EADDDDEDDEGDEVEFFFAFERYFEATERPTTSIATTTTTTTTSESVEFWVRVPTTAASTPDAV 300

Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Dh 301 DKYIETPCDENEHAHEQKAKERI FAKHBERMSQIMBEWEEFAEROAKNI PKADKKAVTQHF 360

Qy 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMMLK 420

DB 361 CEKUTESI ECEB ANERDOLU ETIMADUTAMI NDDDDI AL ENYITAL OAYDDDDDIH EMI K 420

QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA 480

DL-101 HETEROLOGOUS KINETIC STUDIES OF POLYSTYRENE DIVERSIFIED CLANURIN 100

Qy 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
 |||
 Db 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||
 Db 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
 |||
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660

Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697
 |||
 Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697

RESULT 7

ABB78598

ID ABB78598 standard; protein; 697 AA.

XX

AC ABB78598;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human APP695-VF-KK protein sequence SEQ ID NO:20.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
 KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.

DR N-PSDB; ABL52465.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

XX

PS Example 8; Page 120-122; 182pp; English.

XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP695-VF-KK, which
CC is given in an example from the present invention

XX

SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 5; Length 697;
Best Local Similarity 100.0%; Pred. No. 9e-254;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
```

Db 361 QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
 Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
 Qy 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
 Qy 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKKQYTSIHGGV 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKKQYTSIHGGV 660
 Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697

RESULT 8

AAV88428

ID AAV88428 standard; protein; 697 AA.

XX

AC AAV88428;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human APP696-KK amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; APP696-KK.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

PF 23-SEP-1999; 99WO-US020881.

XX

PR 24-SEP-1998; 98US-0101594P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR

N-PSDB; AAA15665.

XX

PT New enzyme designated human aspartase useful in research into Alzheimer's

PT

Disease is capable of cleaving amyloid protein precursor at the beta

PT

secretase site to produce amyloid beta peptide.

XX

Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540
 |||

Db 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||

Db 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIH HGV 660
 |||

Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH HGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
 |||

Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 9

AAU07208

ID AAU07208 standard; protein; 697 AA.

XX

AC AAU07208;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP695-KK.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP695-KK.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.

DR N-PSDB; AAS11708.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

Db	361		QEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421		KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP	480
Db	421		KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP	480
Qy	481		EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE	540
Db	481		EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE	540
Qy	541		DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMD	600
Db	541		DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMD	600
Qy	601		RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSI	660
Db	601		RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSI	660
Qy	661		VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661		VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 10

AAE10635

ID AAE10635 standard; protein; 697 AA.

XX

AC AAE10635;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

DR N-PSDB; AAD17871.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 6; Page 114-116; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by the
CC addition of two Lys residues (KK motif) at the C-terminus of APP695
CC protein

XX

SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 4; Length 697;

Best Local Similarity 99.9%; Pred. No. 2.9e-253;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420

Db	361	QEKVESLEQEAA ¹ NERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP	480
Qy	481	EEIQDEVDELLQKEQNYSD ¹ DLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFS	540
Db	481	EEIQDEVDELLQKEQNYSD ¹ DLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFS	540
Qy	541	DDLQPWHSFGADSV ¹ PANTENEVEPV ¹ DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV ¹ PANTENEVEPV ¹ DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL ¹ VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVM ¹ LKKKQYTSIH ¹ HGV	660
Db	601	RHDSGYEVHHQKL ¹ VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVM ¹ LKKKQYTSIH ¹ HGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 11

AAE06865

ID AAE06865 standard; protein; 697 AA.

XX

AC AAE06865;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein 695-KK (APP695-KK) isoform.

XX

KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
 KW mutein.

XX

OS Homo sapiens.

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

Db	301	 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Db	421	 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS	540
Db	481	 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	 DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Db	601	 RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 12

AAE02587

ID AAE02587 standard; protein; 697 AA.

XX

AC AAE02587;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 695-KK (APP695-KK).

XX

KW Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
therapy; Alzheimer's disease; antialzheimer's.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX


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      |||
Db      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMP SLTETKTTVELLPVNGEFSL 540
Qy      541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      |||
Db      541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIH HGV 660
      |||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH HGV 660
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697
      |||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697

```

RESULT 13

AAU06609

ID AAU06609 standard; protein; 697 AA.

XX

AC AAU06609;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human Amyloid precursor protein mutant, APP695-KK.

XX

KW Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;

KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KW amyloid-beta; Abeta; APP695-KK; mutant; mutein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 696. .697

FT /note= "2 Extra Lys residues added compared to wild-type

FT APP695"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

DR N-PSDB; AAS11523.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Example 6; Page 144-146; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is the human APP695 mutant, APP695-
CC KK which has 2 extra Lys residues added at the C-terminus compared to the
CC wild-type APP695. The mutation alters the specificity of the APP gamma-
CC secretase activity and increases the rate of processing of the amyloid
CC Abeta peptide

XX

SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.9e-253;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
|
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|
Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
|
Db 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db	241	 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 14

ABB78596

ID ABB78596 standard; protein; 697 AA.

XX

AC ABB78596;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human APP695-KK protein sequence SEQ ID NO:16.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 15

AAW19484

ID AAW19484 standard; protein; 695 AA.

XX

AC AAW19484;

XX

DT 08-SEP-1997 (first entry)

XX

DE APP695 mutant A-beta-containing protein.

XX

KW Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;

KW APP.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild-type Val is preferably substituted by Phe"

XX

Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695

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 Job time : 50.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 12:41:23 ; Search time 15 Seconds
(without alignments)
2398.887 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3653	100.0	697	4	US-09-548-372D-20	Sequence 20, Appl
2	3653	100.0	697	4	US-09-548-367D-20	Sequence 20, Appl
3	3653	100.0	697	4	US-09-551-853D-20	Sequence 20, Appl
4	3646	99.8	697	4	US-09-548-372D-16	Sequence 16, Appl
5	3646	99.8	697	4	US-09-548-367D-16	Sequence 16, Appl
6	3646	99.8	697	4	US-09-551-853D-16	Sequence 16, Appl
7	3643	99.7	695	4	US-09-548-372D-14	Sequence 14, Appl
8	3643	99.7	695	4	US-09-548-367D-14	Sequence 14, Appl
9	3643	99.7	695	4	US-09-551-853D-14	Sequence 14, Appl
10	3638	99.6	697	4	US-09-548-372D-18	Sequence 18, Appl
11	3638	99.6	697	4	US-09-548-367D-18	Sequence 18, Appl

12	3638	99.6	697	4	US-09-551-853D-18	Sequence 18, Appl
13	3636	99.5	695	1	US-08-123-702-2	Sequence 2, Appli
14	3636	99.5	695	2	US-08-104-165-1	Sequence 1, Appli
15	3636	99.5	695	3	US-08-464-250-1	Sequence 1, Appli
16	3636	99.5	695	4	US-08-464-250-1	Sequence 1, Appli
17	3636	99.5	695	4	US-09-458-481B-7	Sequence 7, Appli
18	3636	99.5	695	4	US-09-458-481B-8	Sequence 8, Appli
19	3636	99.5	695	4	US-09-548-372D-10	Sequence 10, Appl
20	3636	99.5	695	4	US-09-548-367D-10	Sequence 10, Appl
21	3636	99.5	695	4	US-09-551-853D-10	Sequence 10, Appl
22	3636	99.5	695	4	US-09-415-099-6	Sequence 6, Appli
23	3636	99.5	695	6	5218100-2	Patent No. 5218100
24	3630	99.4	694	1	US-08-339-152A-18	Sequence 18, Appl
25	3630	99.4	694	2	US-08-007-999B-5	Sequence 5, Appli
26	3630	99.4	694	2	US-08-689-276A-5	Sequence 5, Appli
27	3628	99.3	695	4	US-09-548-372D-12	Sequence 12, Appl
28	3628	99.3	695	4	US-09-548-367D-12	Sequence 12, Appl
29	3628	99.3	695	4	US-09-551-853D-12	Sequence 12, Appl
30	3624	99.2	695	1	US-08-371-930-27	Sequence 27, Appl
31	3624	99.2	695	5	PCT-US94-01712-27	Sequence 27, Appl
32	3612	98.9	695	1	US-08-339-152A-30	Sequence 30, Appl
33	3607	98.7	753	4	US-09-548-372D-61	Sequence 61, Appl
34	3607	98.7	753	4	US-09-548-367D-61	Sequence 61, Appl
35	3607	98.7	753	4	US-09-551-853D-61	Sequence 61, Appl
36	3597	98.5	751	1	US-08-123-702-4	Sequence 4, Appli
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40	3597	98.5	751	3	US-08-464-250-2	Sequence 2, Appli
41	3597	98.5	751	4	US-08-464-250-2	Sequence 2, Appli
42	3597	98.5	751	4	US-08-832-867-5	Sequence 5, Appli
43	3597	98.5	751	4	US-09-548-372D-57	Sequence 57, Appl
44	3597	98.5	751	4	US-09-548-367D-57	Sequence 57, Appl
45	3597	98.5	751	4	US-09-551-853D-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-09-548-372D-20

; Sequence 20, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.1e-268;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660

Db 241 EADDDDEDDGDEVEEEAEEPYYEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHGGV 660
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHGGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 3

US-09-551-853D-20

; Sequence 20, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.1e-268;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEF 600
        |||
Db    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVM LKKKQYTSIHHGV 660
        |||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVM LKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697
        |||
Db    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697
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RESULT 4
US-09-548-372D-16
; Sequence 16, Application US/09548372D

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; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-16

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Query Match          99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.8e-267;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
|
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
|
Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|
Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|
Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
|
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
|
Qy    241 EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
|
Db    241 EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
|
Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
|
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
|
Qy    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
|
Db    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

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Qy      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
        |||
Db      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
        |||
Db      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy      541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        |||
Db      541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
        |||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660

Qy      661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
        |||
Db      661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697

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RESULT 5

US-09-548-367D-16

; Sequence 16, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-367D-16

Query Match 99.8%; Score 3646; DB 4; Length 697;

Best Local Similarity 99.9%; Pred. No. 2.8e-267;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

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Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 6

US-09-551-853D-16

; Sequence 16, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-16

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.8e-267;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600

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Db      541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEF 600
Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV 660
          |||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697
          |||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697

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RESULT 7

US-09-548-372D-14

; Sequence 14, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 695

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-372D-14

Query Match 99.7%; Score 3643; DB 4; Length 695;

Best Local Similarity 100.0%; Pred. No. 4.6e-267;

Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG TK 60
          |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG TK 60
Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Db      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
          |||
Db      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEEEE 240

```


Db	181		240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241		300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301		360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361		420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421		480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481		540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541		600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHGGV	660
Db	601		660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	661		695

RESULT 8

US-09-548-367D-14

; Sequence 14, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-14

Query Match 99.7%; Score 3643; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 4.6e-267;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMMLK 420
        |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        |||
Db    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
        |||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
        |||
```

RESULT 9

US-09-551-853D-14

; Sequence 14, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 695

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-14

Query Match 99.7%; Score 3643; DB 4; Length 695;

Best Local Similarity 100.0%; Pred. No. 4.6e-267;

Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||

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Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
 |||

Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
 |||

Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
 |||

Db 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||

Db 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
 |||

Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660

Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 695
 |||

Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 695

RESULT 10

US-09-548-372D-18

; Sequence 18, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-372D-18

Query Match 99.6%; Score 3638; DB 4; Length 697;
 Best Local Similarity 99.6%; Pred. No. 1.1e-266;

	Matches	694;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60							
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60							
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120							
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120							
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180							
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180							
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240							
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240							
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300							
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300							
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360							
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360							
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420							
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420							
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480							
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480							
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540							
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540							
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600							
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVNLD AEF	600							
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITL VMLKKKQYTSIHHGV	660							
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITL VMLKKKQYTSIHHGV	660							
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697							
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697							

RESULT 11

US-09-548-367D-18

; Sequence 18, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 99.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 1.1e-266;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480

```

Qy      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540
          |||
Db      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540

Qy      541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
          |||
Db      541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVNLD AEF 600

Qy      601 RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
          |||
Db      601 RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQNKK 697
          |||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQNKK 697

```

RESULT 12

US-09-551-853D-18

; Sequence 18, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-18

Query Match 99.6%; Score 3638; DB 4; Length 697;

Best Local Similarity 99.6%; Pred. No. 1.1e-266;

Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
          |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy      61 TCIDTKEGILQYQCQEVYP ELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Db      61 TCIDTKEGILQYQCQEVYP ELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

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Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
		:	
Db	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLD AEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 13

US-08-123-702-2

; Sequence 2, Application US/08123702

; Patent No. 5604131

; GENERAL INFORMATION:

; APPLICANT: Wadsworth, Samuel

; APPLICANT: Snyder, Benjamin

; APPLICANT: Reddy, Vermuri, B.

; APPLICANT: Wei, Chamer

; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770

; Patent No. 5604131

; TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:


```

; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-104-165-1

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Query Match          99.5%; Score 3636; DB 2; Length 695;
Best Local Similarity 99.9%; Pred. No. 1.6e-266;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEEE 240
        |||
Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEEE 240

Qy      241 EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV 300
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        |||
Db      361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA 480
        |||
Db      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA 480

Qy      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS 540
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Db      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS 540

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Qy 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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 Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
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 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
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 Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 695
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 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 695
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RESULT 15

US-08-464-250-1

; Sequence 1, Application US/08464250

; Patent No. 6107542

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,250

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/104,165

; FILING DATE: 21-JAN-1992

; APPLICATION NUMBER: 9101307.8

; FILING DATE: 21-JAN-1991

; APPLICATION NUMBER: 9118445.7

; FILING DATE: 28-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joe

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 16163-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 695 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-250-1

Query Match 99.5%; Score 3636; DB 3; Length 695;
Best Local Similarity 99.9%; Pred. No. 1.6e-266;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
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Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        |||
Db    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

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Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Search completed: July 26, 2004, 12:48:23
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 12:40:23 ; Search time 13.6667 Seconds
(without alignments)
4905.768 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QONGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3636	99.5	695	1	A49795	Alzheimer's diseas
2	3585.5	98.2	770	1	QRHUA4	Alzheimer's diseas
3	3539	96.9	695	2	S00550	Alzheimer's diseas
4	3514	96.2	695	2	A27485	Alzheimer's diseas
5	3098	84.8	747	2	JH0773	Alzheimer's diseas
6	2105	57.6	484	4	A32761	hypothetical Alzhe
7	1723	47.2	763	2	A49321	amyloid beta (A4)
8	1711	46.8	765	2	S42880	amyloid precursor-
9	1699	46.5	751	2	A49974	beta-amyloid precu
10	1180	32.3	653	2	A46362	amyloid precursor-
11	1138	31.2	511	2	JC1404	CDEI-box DNA-bindi
12	816.5	22.4	686	2	T15795	hypothetical prote
13	754	20.6	886	2	A32758	beta-amyloid-like

14	706	19.3	246	2	S38344	CDEI-binding prote
15	406	11.1	82	2	PQ0438	Alzheimer's diseas
16	291.5	8.0	191	2	A35981	sperm membrane pro
17	278	7.6	57	2	E60045	Alzheimer's diseas
18	278	7.6	57	2	F60045	Alzheimer's diseas
19	278	7.6	57	2	G60045	Alzheimer's diseas
20	278	7.6	57	2	D60045	Alzheimer's diseas
21	278	7.6	57	2	A60045	Alzheimer's diseas
22	278	7.6	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	185.5	5.1	407	1	EDBEQ3	immediate-early pr
26	184	5.0	5170	2	T15348	hypothetical prote
27	182	5.0	522	2	T32444	hypothetical prote
28	180.5	4.9	993	2	S49461	synaptonemal compl
29	179.5	4.9	1188	2	T46608	zinc finger protei
30	175.5	4.8	802	1	S48529	NAB3 protein - yea
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelsolin-related p
35	174	4.8	1271	2	A45555	glutamate rich pro
36	173.5	4.7	793	1	JH0628	caldesmon - human
37	173	4.7	1187	2	T46637	transcription fact
38	172	4.7	771	1	A33430	h-caldesmon - chic
39	172	4.7	784	2	PN0009	neurofilament trip
40	172	4.7	1182	2	T30189	myelin transcripti
41	169.5	4.6	298	1	TPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	168.5	4.6	675	2	T03744	myoD protein inhib
45	168.5	4.6	913	2	T52485	neurofilament prot

ALIGNMENTS

RESULT 1

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C;Species: *Macaca fascicularis* (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A49795

R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.

A;Reference number: A49795; MUID:91273117; PMID:1905108

A;Accession: A49795

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-695 <POD>

A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

Query Match 99.5%; Score 3636; DB 1; Length 695;
Best Local Similarity 99.9%; Pred. No. 4e-184;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
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Db    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
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RESULT 2

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775

A;Accession: S02260

A;Molecule type: DNA

A;Residues: 1-288, 'V', 365-770 <LEM1>

A;Cross-references: EMBL:X13466

A;Note: alternative splice form APP(695)

R;Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A;Reference number: S05194

A;Accession: S05194

A;Molecule type: DNA

A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>

A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360

A;Note: alternative splice form APP(695)

R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.

A;Reference number: A32277; MUID:89165870; PMID:2538123

A;Accession: A32277

A;Molecule type: DNA

A;Residues: 1-75 <LAF>

A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074

R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.

A;Reference number: A33260; MUID:89392030; PMID:2675837

A;Accession: A33260

A;Molecule type: DNA

A;Residues: 656-737 <JOH>

A;Cross-references: GB:M29270; NID:gl78863; PIDN:AAA51768.1; PID:gl78865

R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.

A;Reference number: A35486; MUID:90321244; PMID:2196878
 A;Accession: A35486
 A;Molecule type: DNA
 A;Residues: 672-710 <PRE1>
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A;Reference number: I39451; MUID:90236318; PMID:2110105
 A;Accession: I39452
 A;Status: nucleic acid sequence not shown; translation not shown; translated
 from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-770 <YOS1>
 A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A;Accession: I39451
 A;Status: nucleic acid sequence not shown; translation not shown; translated
 from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
 A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A;Reference number: A59020; MUID:91340168; PMID:1908403
 A;Contents: annotation; erratum
 A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.;
 van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral
 hemorrhage, Dutch type.
 A;Reference number: I39453; MUID:90260663; PMID:2111584
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary
 Alzheimer's disease.
 A;Reference number: I59562; MUID:92022553; PMID:1925564
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 689-716,'F',718-737 <MUR>
 A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.;
 Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.;
 Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma,
 V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.;
 Schellenberg, G.D.
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds
 for the APP gene region.
 A;Reference number: A44017; MUID:93035397; PMID:1415269

A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692, 'G', 694-718 <KAM1>
 A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A;Experimental source: familial Alzheimer disease family LIT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B. Nature 325, 733-736, 1987
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288, 'V', 365-770 <KAN>
 A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
 A;Reference number: A29030; MUID:87231971; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C. Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756, 'S', 758-770 <GOL>
 A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L. Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K. EMBO J. 7, 949-957, 1988

A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYZ>
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344,'I',365-366 <TAN2>
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
 A;Reference number: S00925; MUID:88122639; PMID:2893289
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344,'I',365-770 <PO2>
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-770 <VIT1>
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288,'V',365-770 <VIT2>
 A;Accession: C30320
 A;Status: not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 2.1e-181;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVR----- 288
      |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    289 ----- 288

Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD 360

Qy    289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
      :|||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

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Qy 406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
 |||
 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 466 MNQSLSLLYNVPAAVEEQDEVDLLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 525
 |||
 Db 541 MNQSLSLLYNVPAAVEEQDEVDLLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

Qy 526 KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 585
 |||
 Db 601 KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
 |||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
 |||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770

RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.;

Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.

A;Reference number: S00550; MUID:88312583; PMID:2900758

A;Accession: S00550

A;Molecule type: mRNA

A;Residues: 1-695 <SHI>

A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617

R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.

A;Reference number: A41245; MUID:88264430; PMID:2968652

A;Accession: A41245

A;Molecule type: protein

A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A;Note: evidence for heparan sulfate attachment

R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.

A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites

A;Note: rat peptides were isolated but not sequenced

R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.

F;625-648/Domain: transmembrane #status predicted <TMM>

Matches 675; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDSIDSADAEEDSDVWVGADTDYADGGEDKVVEVAEEEEVADVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EAEDDEDVEDGDEVEEEAEEPYYEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK	420
Db	361	QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLOPWHPPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600


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Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
      |||:|||||
Db      601 GHDSGFVVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660

Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      |||
Db      661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEOMON 695

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RESULT 4

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 13-Aug-1999

C;Accession: A27485; S19727; I49485

R; Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A;Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085

A;Experimental source: brain

R; de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A;Reference number: S19727; MUID:92096458; PMID:1756177

A;Accession: S19727

A;Molecule type: mRNA

A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695
<STR>

A:Cross-references: EMBL:X59379

R; Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A;Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A:Residues: 1-19 <RES>

A;Cross-references: GB:D10603; NID:q220328; PIDN:BAA01456.1; PID:q220329

C:Genetics:

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A;Map position: 16C3
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 96.2%; Score 3514; DB 2; Length 695;

Best Local Similarity 96.7%; Pred. No. 1.1e-177;

Matches 672; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

[illegible]

A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3098; DB 2; Length 747;
Best Local Similarity 80.9%; Pred. No. 9.2e-156;
Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

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Qy      17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWSDPSGKTCTCIDTKEGILQYCQE 75
      |||| ||| ||||||||| |||||||||::| || || |||||||||
Db      15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy      76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
      |||||||||:|||||:| |:|||||||||||||||
Db      72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy     136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
      |||||:|||||||:|||| |:|:||||||||||||||| |||::
Db     132 LHQERMDICETHLHWHTVAKESCSSEKSMLEHYGMLLPCGIDKFRGVEFVCCPSAEES 191

Qy     196 VDSADAEEDSDVWVGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDDEDDEDGDE 253
      ||||| ||| ||||||| || | |:| || || |||| | |||| | |||
Db     192 FDSADAEEDDCDVWVGADADYVDRSDDKAVEAQPDEEEVVEVEEEETDDDED--DGDE 249

Qy     254 VEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVR----- 288
      ||| |||||||||||||||||||||||||
Db     250 AEEPEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy     289 -----VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
      :| ||||||||| | |||| |
Db     310 SKCAQFIYGGCGGNRNNFESDDYCMVCGSVIPATAASTPDAVDKYLENPNDENEHDFL 369

Qy     318 KAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQ 377
      ||||| |||:|:|:|:|||||||||||||||||||||:|
Db     370 KAKERLEGKHREKMSQVMKEWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy     378 LVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
      |||||||||:||||||| |||||||||||||||||
Db     430 LVETHMARVEAMLNDRRLALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy     438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
      ||||||||| ||||| |||| | ||||||||| |||||
Db     490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPVAVAEEIQDEVDELQKEQNY 549

Qy     498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFLDDLPWHSFGADSVPAN 557
      |||::|:|:| |:| |||||||||:|||||||:|:|:| |||||
Db     550 SDDMVSNMVS DHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLPWHSFGVDSVPAN 609

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Qy      558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
          |||||||||||||||||||||||||||||||||||:|:|:|: |||||||||||
Db      610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy      618 EDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKM 677
          |:||||||||||||||||||||| |||||||||||:|||||||||:||||
Db      670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHGGVVEVDAAVTPEERHLTKM 729

Qy      678 QQNGYENPTYKFFEQMQN 695
          |||||||||||||||
Db      730 QQNGYENPTYKFFEQMQN 747

```

RESULT 6

A32761

hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996

C;Accession: A32761

R;de Sauvage, F.; Octave, J.N.

Science 245, 651-653, 1989

A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted protein.

A;Reference number: A32761; MUID:89346754; PMID:2569763

A;Accession: A32761

A;Molecule type: mRNA

A;Residues: 1-484 <DES>

A;Cross-references: GB:M28373

A;Note: the authors translated the codon ATG for residue 433 as Leu

C;Comment: This is the hypothetical translation of a sequence believed to contain cloning artifacts.

C;Keywords: cloning artifact

```

Query Match          57.6%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 1e-103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

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Qy      80 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGFEFVSDALLVPDKCKFLHQE 139
          |||||||||||||||||||||||||||||||||||
Db      1  LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGFEFVSDALLVPDKCKFLHQE 60

Qy     140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 199
          |||||||||||||||||||||||||||||||||||
Db      61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy     200 DAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDEDGEDGVEVEEEAE 259
          |||||||||||||||||||||||||||||||||||
Db     121 DAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDEDGEDGVEVEEEAE 180

Qy     260 EPYEEATERTTSIATTTTTTTTESVEEVVR----- 288
          |||||||||||||||||||
Db     181 EPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFVDTEGKCAPF 240

Qy     289 -----VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
          :|||||||||||||||||
Db     241 FYGGCGGNRNNFDTEEYCMAVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300

```

Qy 324 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHM 383
 |||
 Db 301 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHM 360

Qy 384 ARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 443
 |||
 Db 361 ARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 420

Qy 444 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEV 487
 |||
 Db 421 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEV 464

RESULT 7

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, D.C.

Biochemistry 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a multigene family.

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney

R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.

submitted to the EMBL Data Library, April 1993

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor like protein.

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA

A;Residues: 1-763 <VON>

A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764

R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Neve, R.L.; Tanzi, R.E.

Nature Genet. 5, 95-99, 1993

A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's associated amyloid beta protein precursor.

A;Reference number: S40519; MUID:94035131; PMID:8220435

A;Accession: S40519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <WAS>

A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392

C;Genetics:

A;Gene: GDB:APLP2; APPL2

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;

Qy	5	LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRNLNMHNVQNGKWDSDP	56
Db	15	LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD	74
Qy	57	SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
Db	75	TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK	132
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
Db	133	CLVGEFVSDVLLVPEKQCFHKKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV	192
Qy	177	DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE	236
Db	193	DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD	245
Qy	237	VEE--EEA--DDDEDDDEDGVEVEEAEPY-----EEATERTTSIATTTTTTTTES	282
Db	246	LEDFTEAAVDEDDDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD	305
Qy	283	VEEV-----VRVP	290
Db	306	VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKAMIP	365
Qy	291	TTAASTPDAVDKYLETPGDENEHAHFQAKAKERLEAKHRERMSQVMREWEAAERQAKNLPK	350
Db	366	PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNMRMDRVKKEWEEAELQAKNLPK	424
Qy	351	ADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRLALENYITALQAVPP	410
Db	425	AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP	484
Qy	411	RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQL	470
Db	485	RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMSQVMTHLVIEERRNQL	544
Qy	471	SLLYNVPAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVE	530
Db	545	SLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISETPVDVR	587
Qy	531	LLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN-----	585
Db	588	---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL	635
Qy	586	IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----NKG	625

Db 636 IGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEEERESVGPLREDFSLSSS 693

Qy 626 AIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENP 685
|:|:|:| | | | | | |:|:|:|:|:|:| |:|:|:|:| |:|:|:|:| |:|:|:|:|

Db 694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYENP 753

Qy 686 TYKFFEQMQ 694
|:|:|:| | | | |

Db 754 TYKYLEQMQ 762

RESULT 8

S42880

amyloid precursor-like protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999

C;Accession: S42880; S47528

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.

submitted to the EMBL Data Library, March 1994

A;Description: Complete nucleotide and deduced amino acid sequence of rat amyloid precursor-like protein 2 (Aplp2/Apph): Two amino acids length difference to human and murine homologues.

A;Reference number: S42880

A;Accession: S42880

A;Molecule type: mRNA

A;Residues: 1-765 <SAN>

A;Cross-references: EMBL:X77934

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.

Biochim. Biophys. Acta 1219, 167-170, 1994

A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor-like protein 2 (APLP2/APPH): two amino acids length difference to human and murine homologues.

A;Reference number: S47528; MUID:94368849; PMID:8086458

A;Accession: S47528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-765 <SA2>

A;Cross-references: EMBL:X77934

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 1711; DB 2; Length 765;

Best Local Similarity 46.1%; Pred. No. 1e-82;

Matches 363; Conservative 122; Mismatches 167; Indels 136; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
|:|:|:| | | | | |:|:|:|:|:|:| |:|:|:|:| |:|:|:|:| |:|:|:|:|

Db 15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy 57 SGTKTCTIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
:|:|:|:|:| |:|:|:|:|:|:|:|:|:|:| |:|:|:|:|:|:| |:|:|:|:|:|:|

Db 75 TGTKSCLGTKEEVLYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
|:|:|:|:|:| |:|:|:|:|:|:|:|:|:|:| |:|:|:|:|:|:| |:|:|:|:|:|:|

J. Biol. Chem. 269, 2637-2644, 1994

A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid precursor protein (APP).
A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.5%; Score 1699; DB 2; Length 751;
Best Local Similarity 45.8%; Pred. No. 4.2e-82;
Matches 362; Conservative 113; Mismatches 160; Indels 156; Gaps 20;

```

Qy      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
      | :|||  || | :          |||  :|:|:|:|:|:|:|:|:|:|  ||: ||
Db      15 LLVLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy      57 SGTKTCTIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :||:|: ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|  | :||:| :|:|:|  | ||:|
Db      75 TGTKSCLGTKEEVLQYQCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy     117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      |||:|:| ||| | :| |||:|:| | ||: || | :  | : |||:|:|:
Db     133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSGMLLPCGV 192

Qy     177 DKFRGVEFVCCPLAE--ESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEVAE---E 231
      |:| | |:|:| :  :||: | : ||:|  | | ||  : : | |
Db     193 DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLDKSEFPTE 243

Qy     232 EEVAEVEEEEEAD-DEDEDGDEVEEE-----AEPYEEATERTTTSIATTT 276
      :: : | || :|:|:|:|:| | :  | | | : : | | |
Db     244 ADLEDFTAAADEEEEEDEEEGEEVVEDRDYYYDPFKGDDYNEENPTSPSSEGTIS----- 298

Qy     277 TTTTESVEEV----- 286
      | | :|
Db     299 --DKEIVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYC 356

Qy     287 -----VRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
      :| |  | | | | | | | :|:| | | | :| | | :| :|:| |
Db     357 MAVCKAMIPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEA 415

Qy     342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRRLALENY 401
      | | | | | | : : : | | | | :|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     416 ELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRRLALENY 475

Qy     402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRV 461
      : | |:| | | | :  | :|:|:| | | | :|:|:|:| | | :|:|:|:|:|:| |
Db     476 LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV 535

Qy     462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPS 521
      | | | | | | | | | | | :|:|:|:|:|:|:|:|:|:|  | :|  | |
Db     536 IEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTSS 578

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Qy      522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGS 581
          :| | : | : | | | : : || | : : |
Db      579 ISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQDG- 621

Qy      582 GLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----N 623
          || : : | | : || | : | : : : | | | | :
Db      622 GLIGAEKVIN SKNKM DENMVIDETLDV--KEMIFNAERVGGLEEEPE SVGPLREDFSL S 679

Qy      624 KGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYE 683
          | : || : | | | || | : || : : || : | | : || | : || || : || | : || |
Db      680 SNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQN HGYE 739

Qy      684 NPTYKFFEQMQ 694
          || || : || |
Db      740 NPTYKYLEQMQ 750

```

RESULT 10

A46362

amyloid precursor-like protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C;Accession: A46362

R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992

A;Title: Identification of a mouse brain cDNA that encodes a protein related to
the Alzheimer disease-associated amyloid beta protein precursor.

A;Reference number: A46362; MUID:93066322; PMID:1279693

A;Accession: A46362

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-653 <WAS>

A;Experimental source: brain

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

C;Keywords: transmembrane protein

```

Query Match          32.3%;  Score 1180;  DB 2;  Length 653;
Best Local Similarity 38.4%;  Pred. No. 7.4e-55;
Matches 269;  Conservative 121;  Mismatches 232;  Indels 78;  Gaps 17;

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Qy      1  MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMH MNVQNGKWSDSPSGT 59
          :| | | : || | | | | : | : | | | | : : : | : | : | :
Db      22  LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy      60  KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
          : | : : : | : || : : || | | : | : : | | | | : | : | |
Db      81  RRCLLDLPQRVLEYCRQMPYELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy      119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
          | | | | : | | | | : | : | | | | | | : | : | | | | | :
Db      141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQAEACSSQGLILHGSGMLLPCGSDR 200

Qy      179 FRGVEFVCCPLAEESDNVDSADAEEDDSVDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
          | | | | : | | | : | : : | | | : | | | | | | | |

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Db      201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-----EEEVESF 248
Qy      238 EEEEADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTP 297
      : | : :| ||| | : | : : | | ||
Db      249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR-----PT----- 294
Qy      298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVI 357
      | || | ||: || | :|| || : :||| || | :| ||||| :|:
Db      295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354
Qy      358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN 417
      :||| :||:| : | ||:| || | | :||:| || | : | || | |
Db      355 EHFQSIQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLN 414
Qy      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
      | :| :| ||||| :| :||:| || | | ||:| | ||||| | | |
Db      415 ALRRYLRAEQKEQRHTLRHYQHVAVDPEKAQQMRQVQVTHLQVIEERMNQSLGLLDQNP 474
Qy      478 AVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
      :|:|: : : || | | : : | | : | | :| |
Db      475 HLAQELRPQIQELL-----LAEHLGPSEL----DASVPGSSSEDK----- 510
Qy      537 EFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
      || | | :| :| | :| | : | | : : :
Db      511 ----GSLQP-----PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551
Qy      597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKKQ 652
      | : | | : | :| :| :| :| :| :| :| :|
Db      552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSRREALSGLLIMGAGGSLIVLSLLLLRKKKP 611
Qy      653 YTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
      | :| ||||| :| ||: | :| :| ||||| :| | :
Db      612 YGTISHGVVEVDPMLTLEEQLRELQRHGYENPTYRFL EE 651

```

RESULT 11

JC1404

CDEI-box DNA-binding protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997

C;Accession: JC1404

R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.

Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992

A;Title: A murine sequence-specific DNA binding protein shows extensive local similarities to the amyloid precursor protein.

A;Reference number: JC1404; MUID:93129193; PMID:1482349

A;Accession: JC1404

A;Molecule type: mRNA

A;Residues: 1-511 <VID>

C;Comment: This protein plays an important role in the early development of the mouse.

C;Keywords: DNA binding; transmembrane protein

Query Match 31.2%; Score 1138; DB 2; Length 511;

Best Local Similarity 45.6%; Pred. No. 8.9e-53;

Matches 252; Conservative 92; Mismatches 129; Indels 80; Gaps 16;

Qy	174	CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAE-	230
Db	6	CGVDQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLDKSEF	56
Qy	231	--EEEVAEVEEEEEAD-DEDEDDEGDEVEEEAE-----EPYEEATERTTSIATTTTTT	279
Db	57	PTEADLEDFTEAAADEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS	114
Qy	280	TESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWE	339
Db	115	DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE	173
Qy	340	EAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALE	399
Db	174	EAEIQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRIALE	233
Qy	400	NYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL	459
Db	234	NYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHL	293
Qy	460	RVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIM	519
Db	294	HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFT	336
Qy	520	PSLTETKTTVELLPVNGEFSLDDLQPVHSFGADSVPAANTENEVEPVDPARPAADRGLTTRP	579
Db	337	SSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQD	380
Qy	580	GSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----	622
Db	381	G-GLIGAEKVINSKNKMENMVIDETLDV--KEMIFNAERVGGLEEEEPESVGPLREDFS	437
Qy	623	-NKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG	681
Db	438	LSSNALIGLLVIAVAIATVIVISLVMKRKQYGTISHGIVEVDPLMTPEERHLNKMQNHG	497
Qy	682	YENPTYKFFEQMQ	694
Db	498	YENPTYKYLEOMO	510

A;Experimental source: strain Bristol N2; clone C42D8
R;Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human beta-amyloid protein precursor.
A;Reference number: A49414; MUID:94089766; PMID:8265668
A;Accession: A49414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-686 <DAI>
A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C;Genetics:
A;Gene: CESP:C42D8.8
A;Map position: X
A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 22.4%; Score 816.5; DB 2; Length 686;
Best Local Similarity 29.1%; Pred. No. 1.1e-35;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	TK	60
		:: :		
Db	6	LMIGLLIPILVA-TVYAEAGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA		63
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVPIPYRCLVG		120
Db	64	TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG		122
Qy	121	EFVSDALLVDPKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGM		174
Db	123	EFHSEALQVPHDQFQSHVNSRDQCNDYQHWKDEAGQCKTKKSKGNKDMIVRSFAVLEPC		182
Qy	175	GIDKFRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEV		234
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Db	183	ALDMFTGVEFVCCP----NDQTNKTDVQKTK-----		209
Qy	235	AEVEEEEADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVRVPTTAA		294
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Db	210	---EDEDDEDDDAYEDDYSEESDEKDEE-----		236
Qy	295	STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEA-----ERQAKNLP		349
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Db	237	-EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHKRKKVDKVMKEWGDLETRYNEQAKD-P		294
Qy	350	KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL-		405
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Db	295	KGAEKFSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA		354
Qy	406	-QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE		464
Db	355	THVNKPNKHSVLQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL		414
Qy	465	RMNQSLSLLYNVP-----AVA--EEIQDEVDELLQKEQNYSDDLANMISEPRISY		513
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Db      415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPPDISVE----DSELTPIIHDDEFSK 470
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Qy      565 VDARP-----AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
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Qy      599 E-----FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLK 649
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RESULT 13

A32758

beta-amyloid-like protein precursor - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998

C;Accession: A32758

R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.

Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989

A;Title: A *Drosophila* gene encoding a protein resembling the human beta-amyloid protein precursor.

A;Reference number: A32758; MUID:89184650; PMID:2494667

A;Accession: A32758

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-886 <ROS>

A;Cross-references: GB:J04516; NID:g158371; PID:g158372

C;Genetics:

A;Gene: FlyBase:Appl

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C;Keywords: transmembrane protein

Query Match 20.6%; Score 754; DB 2; Length 886;

Best Local Similarity 25.7%; Pred. No. 2.9e-32;

Matches 234; Conservative 127; Mismatches 287; Indels 264; Gaps 29;

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Qy      59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
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Qy      113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
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Qy      173 PCGIDKFRGVEFVCCP-----LAESDNVD---SA 199

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A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

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Best Local Similarity 98.8%; Pred. No. 3.1e-15;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db       61 IVITLVMLKKKQYTSIHGGVVE 82
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Search completed: July 26, 2004, 12:47:29
Job time : 15.6667 secs

OM protein - protein search, using sw model

Run on: July 26, 2004, 12:46:43 ; Search time 44.3333 Seconds
(without alignments)
4923.349 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8			Query	
Result	No.	Score	Match	Length	ID	Description

1	3653	100.0	697	9	US-09-794-927-20	Sequence 20, Appl
2	3653	100.0	697	9	US-09-795-847-20	Sequence 20, Appl
3	3653	100.0	697	9	US-09-794-743-20	Sequence 20, Appl
4	3653	100.0	697	9	US-09-794-748-20	Sequence 20, Appl
5	3653	100.0	697	9	US-09-794-925-20	Sequence 20, Appl
6	3653	100.0	697	9	US-09-681-442-20	Sequence 20, Appl
7	3653	100.0	697	10	US-09-869-414-20	Sequence 20, Appl
8	3653	100.0	697	10	US-09-548-366-20	Sequence 20, Appl
9	3653	100.0	697	12	US-10-652-927-20	Sequence 20, Appl
10	3653	100.0	697	12	US-10-652-830-20	Sequence 20, Appl
11	3646	99.8	697	9	US-09-794-927-16	Sequence 16, Appl
12	3646	99.8	697	9	US-09-795-847-16	Sequence 16, Appl
13	3646	99.8	697	9	US-09-794-743-16	Sequence 16, Appl
14	3646	99.8	697	9	US-09-794-748-16	Sequence 16, Appl
15	3646	99.8	697	9	US-09-794-925-16	Sequence 16, Appl
16	3646	99.8	697	9	US-09-681-442-16	Sequence 16, Appl
17	3646	99.8	697	10	US-09-869-414-16	Sequence 16, Appl
18	3646	99.8	697	10	US-09-548-366-16	Sequence 16, Appl
19	3646	99.8	697	12	US-10-652-927-16	Sequence 16, Appl
20	3646	99.8	697	12	US-10-652-830-16	Sequence 16, Appl
21	3643	99.7	695	9	US-09-794-927-14	Sequence 14, Appl
22	3643	99.7	695	9	US-09-795-847-14	Sequence 14, Appl
23	3643	99.7	695	9	US-09-794-743-14	Sequence 14, Appl
24	3643	99.7	695	9	US-09-794-748-14	Sequence 14, Appl
25	3643	99.7	695	9	US-09-794-925-14	Sequence 14, Appl
26	3643	99.7	695	9	US-09-681-442-14	Sequence 14, Appl
27	3643	99.7	695	10	US-09-869-414-14	Sequence 14, Appl
28	3643	99.7	695	10	US-09-548-366-14	Sequence 14, Appl
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30	3643	99.7	695	12	US-10-652-830-14	Sequence 14, Appl
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32	3638	99.6	697	9	US-09-795-847-18	Sequence 18, Appl
33	3638	99.6	697	9	US-09-794-743-18	Sequence 18, Appl
34	3638	99.6	697	9	US-09-794-748-18	Sequence 18, Appl
35	3638	99.6	697	9	US-09-794-925-18	Sequence 18, Appl
36	3638	99.6	697	9	US-09-681-442-18	Sequence 18, Appl
37	3638	99.6	697	10	US-09-869-414-18	Sequence 18, Appl
38	3638	99.6	697	10	US-09-548-366-18	Sequence 18, Appl
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40	3638	99.6	697	12	US-10-652-830-18	Sequence 18, Appl
41	3636	99.5	695	9	US-09-794-927-10	Sequence 10, Appl
42	3636	99.5	695	9	US-09-795-847-10	Sequence 10, Appl
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44	3636	99.5	695	9	US-09-794-748-10	Sequence 10, Appl
45	3636	99.5	695	9	US-09-794-925-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-794-927-20

; Sequence 20, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-20

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Query Match          100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-795-847-20

; Sequence 20, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-795-847-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-794-743-20
; Sequence 20, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300

Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVM LKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVM LKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697

RESULT 4

US-09-794-748-20

; Sequence 20, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 5

US-09-794-925-20

; Sequence 20, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI

; CURRENT APPLICATION NUMBER: US/09/794,925

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-925-20

Query Match 100.0%; Score 3653; DB 9; Length 697;

Best Local Similarity 100.0%; Pred. No. 2.5e-224;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 6

US-09-681-442-20

; Sequence 20, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI PYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI PYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEF	600
Qy	601	RHD SGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHD SGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 8

US-09-548-366-20

; Sequence 20, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES THEREFOR

; FILE REFERENCE: 28341/6280A

; CURRENT APPLICATION NUMBER: US/09/548,366

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-366-20

Query Match 100.0%; Score 3653; DB 10; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

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Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 9

US-10-652-927-20

; Sequence 20, Application US/10652927

; Publication No. US20040043408A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N3

; CURRENT APPLICATION NUMBER: US/10/652,927

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver.. 2.0

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-652-927-20

Query Match 100.0%; Score 3653; DB 12; Length 697;

Best Local Similarity 100.0%; Pred. No. 2.5e-224;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 10

US-10-652-830-20

; Sequence 20, Application US/10652830

; Publication No. US20040048303A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N1

; CURRENT APPLICATION NUMBER: US/10/652,830

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-830-20

Query Match 100.0%; Score 3653; DB 12; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDDLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDDLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        |||
Db    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV 660
        |||
Db    601 RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
        |||
```

RESULT 11

US-09-794-927-16

; Sequence 16, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/794,927

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-927-16

Query Match 99.8%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.9%; Pred. No. 7.1e-224;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYQCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYQCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHD SGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITL VMLKKKQYTSIHHGV	660
Db	601	RHD SGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITL VMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697

RESULT 12

US-09-795-847-16

; Sequence 16, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER:  PCT/US99/20881
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  60/101,594
; PRIOR FILING DATE:  1998-09-24
; NUMBER OF SEQ ID NOS:  73
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-795-847-16
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Db          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
Qy          661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
           |||
Db          661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697

```

RESULT 13

US-09-794-743-16

; Sequence 16, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-743-16

Query Match 99.8%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.9%; Pred. No. 7.1e-224;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
           |||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
Qy          61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
           |||
Db          61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy          121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
           |||

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Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
 |||

Db 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
 |||

Db 241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
 |||

Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
 |||

Db 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480
 |||

Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480

Qy 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540
 |||

Db 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||

Db 541 DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITL VMLKKKQYTSIHHGV 660
 |||

Db 601 RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITL VMLKKKQYTSIHHGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
 |||

Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 14

US-09-794-748-16

; Sequence 16, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 7.1e-224;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540

Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI PYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDEDGDEVEEEAEEPYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK	697

Search completed: July 26, 2004, 13:00:45
 Job time : 46.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 12:39:53 ; Search time 35.3333 Seconds
(without alignments)
6224.043 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	3423	93.7	695	13	Q9DGJ8	Q9dgj8 gallus gall
2	3382	92.6	751	13	Q9DGJ7	Q9dgj7 gallus gall
3	3209	87.8	693	13	Q98SG0	Q98sg0 xenopus lae
4	3185	87.2	695	13	Q98SF9	Q98sf9 xenopus lae
5	3183	87.1	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
6	3098	84.8	747	13	Q91963	Q91963 xenopus. ap
7	2959.5	81.0	699	13	O57394	O57394 narke japon
8	2762.5	75.6	569	13	Q9PVL1	Q9pvl1 gallus gall
9	2608	71.4	534	13	O93296	O93296 gallus gall
10	2562	70.1	678	13	Q7ZZT1	Q7zzt1 brachydanio
11	2524	69.1	738	13	Q90W28	Q90w28 brachydanio
12	2482.5	68.0	694	13	Q8UUR9	Q8uur9 brachydanio
13	2334	63.9	612	13	Q9I9E7	Q9i9e7 brachydanio
14	1923	52.6	384	11	Q8BPC7	Q8bpc7 mus musculu
15	1757	48.1	695	4	Q13861	Q13861 homo sapien
16	1744.5	47.8	669	4	Q14662	Q14662 homo sapien
17	1739	47.6	707	11	Q80US7	Q80us7 mus musculu
18	1735	47.5	695	11	Q64348	Q64348 mus musculu
19	1726	47.2	715	11	Q7TT34	Q7tt34 mus musculu
20	1703	46.6	763	11	Q61482	Q61482 mus musculu
21	1699	46.5	751	11	Q60709	Q60709 mus musculu
22	1650	45.2	472	13	Q8UUS0	Q8uus0 brachydanio
23	1345.5	36.8	357	13	Q8UUI8	Q8uui8 brachydanio
24	1296.5	35.5	522	4	Q9BT36	Q9bt36 homo sapien
25	1085	29.7	218	11	Q8BPV5	Q8bpv5 mus musculu
26	1043.5	28.6	523	4	Q14594	Q14594 homo sapien
27	790	21.6	357	13	Q7ZZT2	Q7zzt2 brachydanio
28	766	21.0	239	13	Q8UUI7	Q8uui7 brachydanio
29	572	15.7	113	13	Q8JH58	Q8jh58 chelydra se
30	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
31	478	13.1	97	6	Q28673	Q28673 oryctolagus
32	435.5	11.9	140	13	Q800X9	Q800x9 chelydra se
33	396.5	10.9	82	4	Q16014	Q16014 homo sapien
34	390.5	10.7	82	4	Q16019	Q16019 homo sapien
35	387.5	10.6	82	4	Q16020	Q16020 homo sapien
36	371	10.2	79	11	O35463	O35463 cricetulus
37	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
38	330	9.0	208	11	Q8R0R7	Q8r0r7 mus musculu
39	234	6.4	49	6	O97917	O97917 bos taurus
40	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
41	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
42	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
43	192.5	5.3	1110	13	Q91255	Q91255 petromyzon
44	191.5	5.2	556	5	Q9V7I9	Q9v7i9 drosophila
45	188	5.1	785	5	Q9GQ82	Q9gq82 drosophila

ALIGNMENTS

RESULT 1

Q9DGJ8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 93.7%; Score 3423; DB 13; Length 695;
Best Local Similarity 93.8%; Pred. No. 1.5e-198;
Matches 654; Conservative 17; Mismatches 22; Indels 4; Gaps 3;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKLLHQRMDVCEETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVE--VAEEEEVAEVE 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDNLDSADAEEDDSVWVGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy    239 EEEADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
      |:||| |:||| |:||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db    241 DEDADD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298

Qy    299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQ 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQ 358

Qy    359 HFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNM 418
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    359 HFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQTVPPRPRHVFNM 418

```

Qy 419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
 |||
 Db 419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478
 Qy 479 VAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVNGEF 538
 |||:|
 Db 479 VAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTTVELLPVDGEF 538
 Qy 539 SLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
 |||:|:|
 Db 539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVESEVKMDA 598
 Qy 599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHH 658
 |||
 Db 599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
 Qy 659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 695
 |||
 Db 659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 695

RESULT 2

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
 AC Q9DGJ7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF289219; AAG00594.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.

Db 659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVE 718

Qy 663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
 ||| |

Db 719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751

RESULT 3

Q98SG0

ID Q98SG0 PRELIMINARY; PRT; 693 AA.
 AC Q98SG0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -.
 DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 87.8%; Score 3209; DB 13; Length 693;
 Best Local Similarity 87.7%; Pred. No. 1.2e-185;
 Matches 611; Conservative 36; Mismatches 44; Indels 6; Gaps 4;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
 ||| : ||:| | |||| | | ||||| ||||| : ||||| : |||||

Db 1 MLPHITLLVLTIV-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
 || ||||| : ||||| : ||||| : |||||

Db 60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPIYRCLVG 119

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 ||||| : ||||| : ||||| : |||||

Db 120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMLEHYGMLLPCGIDKFR 179

Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEVA--EEEEVAEVE	238
Db	180	GVEFVCCPSAEESFSADSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEEEEVVEVE	238
Qy	239	EEEADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTSESVEEVVRVPTTAASTPD	298
Db	239	EEETDDDED--DGDEAEPEPEPEYEEATERTTSIATTTTTTTTSESVEEVVRVPATAASTPD	296
Qy	299	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQ	358
Db	297	AVDKYLENPNDENEHDFLAKAKERLEGKHREKMSQVMKEWEEAERQAKNLPKADKKAVIQ	356
Qy	359	HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM	418
Db	357	HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNM	416
Qy	419	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA	478
Db	417	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA	476
Qy	479	VAEEIQDEVDDELLOKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF	538
Db	477	VAEEIQDEVDDELFOKEQNYSDDMVSNMVSDFRVSYGNDALMPSLSETKTTVELLPVDGEF	536
Qy	539	SLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA	598
Db	537	NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS	596
Qy	599	EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHH	658
Db	597	EYRHDTAYEVHHQKLVFFAEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH	656
Qy	659	GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	657	GVVEVDAAVTPEERHLTKMOONGYENPTYKFFEMON	693

DR EMBL; AJ298151; CAC37194.1; -.
 DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 87.2%; Score 3185; DB 13; Length 695;
 Best Local Similarity 87.1%; Pred. No. 3.5e-184;
 Matches 608; Conservative 39; Mismatches 45; Indels 6; Gaps 5;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
		:	
Db	1	MLPHITLLVLTALGALALEVPADGNGLLAEPQIAMFCGRLNMHMNVQNGKWETDVS	59
Qy	61	TCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Db	60	GCIGTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKSRTHIVVP	119
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPC	180
Db	120	EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPC	179
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEV--AE	238
Db	180	GVEFVCCPTAEESFSDADA-EDSDVWVGADADYVDRSDDKAVEAQPEEE	238
Qy	239	EEEADDDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-V	297
Db	239	EEEADDD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVR	297
Qy	298	DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLP	357
Db	298	DAVDKYLENPNDENEHDFLKAERLEKGRHREKMSQVMKEWEEAERQAKNLP	357
Qy	358	QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPP	417
Db	358	QHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYITALQADPP	417
Qy	418	MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIYERMN	477
Db	418	MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVINERMN	477
Qy	478	AVAEIQDEVDLQKEQNYSDVLNMISEPRISYGNALMPSLTETKTTVELLP	537
Db	478	AVAEIQDEVDLQKEQNYSDVMVSNMVSDFRVSYGNALMPSLTSETKTTVELLP	537
Qy	538	FSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSLTNIKTEE	597

Db	538	FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD	597
Qy	598	AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIH	657
Db	598	SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTTIH	657
Qy	658	HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	695
Db	658	HGVVEVDAAVTPEERHLTKMOONGYENPTYKFFEOMON	695

07ZX00

Query Match 87.1%; Score 3183; DB 13; Length 695;
Best Local Similarity 87.1%; Pred. No. 4.6e-184;
Matches 608; Conservative 38; Mismatches 46; Indels 6; Gaps 5;

```

Db      120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179
Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEV--AEEEEVAEVE 238
      ||||| ||||: |||| ||||| || | :|| || |||| |||
Db      180 GVEFVCCPTAEESFDSADA-EDSDVWVGADADYVDRSDDKAVEAQPEEEEEVVEVE 238
Qy      239 EEEADDEDEDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
      ||||| ||: |||| || ||||| ||||| ||||| || || |||
Db      239 EEEADDD-DDDDGDETEEEPEEPEYEATERTTSIATTTTTTTESVEEVVRVPATAVSTP 297
Qy      298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVI 357
      ||||| || |||| | ||||| ||||: ||: ||: ||||| |||||
Db      298 DAVDKYLENPNDENEHDFLKAERLEGGHREKMSQVMKEWEEAERQAKNLPKADKKAVI 357
Qy      358 QHFQEKVESLEQEAAERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      358 QHFQEKVESLEQEAAERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417
Qy      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477
Qy      478 AVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTETKTTVELLPVNGE 537
      ||||| ||||| ||||| ||||: ||: ||: ||: ||||| ||||: ||||| ||||: ||
Db      478 AVAEEIQDEVDELQKEQNYSDVMVSNMVS DHRVSYGNLMPSLSETKTTVELLPVDGE 537
Qy      538 FSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
      |: |: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597
Qy      598 AEFRHDSGYEVHHQKL VFFAEDEVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIH 657
      |: |: ||: ||||| ||||: ||||: ||||: ||||: ||||: ||||: ||
Db      598 SEYRHDAAYEVHHQKL VFFAEDEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657
Qy      658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      ||||| ||||| ||||: ||||| ||||| |||||
Db      658 HGVVEVDAAVTPEERHLTKMQNGYENPTYKFFEQMQN 695

```

RESULT 6

Q91963

```

ID   Q91963      PRELIMINARY;          PRT;    747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;

```

RA Okado H., Okamoto H.;
 RT "A Xenopus homologue of the human beta-amyloid precursor protein:
 RT developmental regulation of its gene expression.";
 RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
 DR EMBL; S52417; AAB24853.1; -.
 DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 84.8%; Score 3098; DB 13; Length 747;
 Best Local Similarity 80.9%; Pred. No. 6.9e-179;
 Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE	75
Db	15	ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF	135
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF	131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEEEDN	195
Db	132	LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES	191
Qy	196	VDSADAEEDSDVWVGADTDYADGSEDKVVEVA---EEEEVAEVEEEEADDDDEDGEDGDE	253
Db	192	FDSADAAEDDCDVWVGADADYVDRSDDKAVEAQPDEEEVVEVEEEEETDDDED--DGDE	249
Qy	254	VEEEAEEPVEEATERTTSIATTTTTTTTSESVEEVVR-----	288
Db	250	AEEPEEPVEEATERTTSIATTTTTTTTSESVEEVVREVCSEAETGPCRAMISRWYYDVTE	309
Qy	289	-----VPTTAASTPDAVDKYLETPGDENEHAHFQ	317
		:	
Db	310	SKCAQFIYGGCGGNRNNFESDDYCMVCGSVIPATAASTPDAVDKYLENPNDENEHDFL	369
Qy	318	KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQ	377
Db	370	KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ	429

Qy 378 LVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHf 437
 |||:||||| |||
 Db 430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHf 489
 Qy 438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNY 497
 ||| ||| |||
 Db 490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAAVEEIQDEVDELQKEQNY 549
 Qy 498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
 |||::||:| |:|||||:|||||:||::||| |||
 Db 550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609
 Qy 558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
 |||:|||||:|||||:|||||:|||||: |||
 Db 610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669
 Qy 618 EDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKM 677
 |:|||||:|||||:|||||:|||||:|||||: ||
 Db 670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHGGVVEVDAAVTPEERHLTKM 729
 Qy 678 QQNGYENPTYKFFEQQMN 695
 |||
 Db 730 QQNGYENPTYKFFEQQMN 747

RESULT 7

O57394

ID O57394 PRELIMINARY; PRT; 699 AA.
 AC O57394;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE EL amyloid precursor protein 699.
 GN EL APP699.
 OS Narke japonica (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hypnosqualia; Pristiorajae; Batoidea;
 OC Torpediniformes; Narcinoidei; Narkidae; Narke.
 OX NCBI_TaxID=62965;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Electric lobe;
 RX MEDLINE=98129705; PubMed=9461486;
 RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
 RA Suzuki T.;
 RT "cDNA isolation of Alzheimer's amyloid precursor protein from
 RT cholinergic nerve terminals of the electric organ of the electric
 RT ray.";
 RL Biochem. J. 330:29-33(1998).
 DR EMBL; AB005544; BAA24230.1; -.
 DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.

O9PVL1

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ID      Q9PVL1      PRELIMINARY;      PRT;      569 AA.
AC      Q9PVL1;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Amyloid protein (Fragment).
GN      APP.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT      "What the evolution of the amyloid protein precursor supergene family
RT      tells us about its function.";
RL      Neurochem. Int. 0:0-0(2000).
DR      EMBL; AF030341; AAF12698.1; -.
DR      HSSP; P05067; 1BA4.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
FT      NON_TER      1      1
SQ      SEQUENCE      569 AA;      64753 MW;      0AB8BB851863A19D CRC64;

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Query Match 75.6%; Score 2762.5; DB 13; Length 569;
Best Local Similarity 93.4%; Pred. No. 8.9e-159;
Matches 534; Conservative 14; Mismatches 19; Indels 5; Gaps 4;

Qy	126	ALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFV	185
		:	
Db	1	ALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLSCGIDKFRGVEFV	60
Qy	186	CCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEEEEEEAD	243
		: : : : : :	
Db	61	CCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVEDEDAD	120
Qy	244	DDEDEDGDVEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAVDKY	303
		: :	
Db	121	DD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDVVDKY	178
Qy	304	LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEK	363
Db	179	LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAEROAKNLPKADKKAVIQHFQEK	238

QY 364 VESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYV 423
 |||:|||||
 Db 239 VESLEQEAAANERQQLVETHMARVEAMLNDRRIAENYITALQTVPPRPRHVFNMLKKYV 298
 QY 424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEEI 483
 |||:|||||
 Db 299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEEI 358
 QY 484 QDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFLDDL 543
 |||:|||||
 Db 359 QDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPTLTETKTTVELLPVNGEFLDDL 418
 QY 544 QPWSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603
 |||||:|||||
 Db 419 QPWHFPGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTTEEVEVKMDAEFRHD 478
 QY 604 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGVEV 663
 |||:|||||
 Db 479 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHGVEV 538
 QY 664 DAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
 |||||
 Db 539 DAAVTP-ERHLSKMQQNGYENPTYKFFEQQMN 569

RESULT 9

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.
 AC O93296;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 RT substrate for caspase-3 in dying motoneurons."
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL; AF042098; AAC25052.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 71.4%; Score 2608; DB 13; Length 534;
Best Local Similarity 94.6%; Pred. No. 1.8e-149;
Matches 505; Conservative 13; Mismatches 12; Indels 4; Gaps 3;

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Qy      164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSED 223
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3  NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWVGADADYADGSDD 62

Qy      224 KVVE--VAEEEEVAEVEEEEADDDDEDEDGDEVEEEAEOPYEEATERTTSIATTTTTTTE 281
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTE 120

Qy      282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy      342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRLALENY 401
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRIALENY 240

Qy      402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy      462 IYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPS 521
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 IYERMNQSLSFLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPS 360

Qy      522 LTETKTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS 581
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361 LTETKTTVELLPVDGEFLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy      582 GLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      421 GLTNVKTEEVSSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy      642 FITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      481 VITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 534
```

RESULT 10

Q7ZZT1

ID Q7ZZT1 PRELIMINARY; PRT; 678 AA.

AC Q7ZZT1;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Amyloid protein a variant 2.

GN APPA.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RT "Investigation of zebrafish appa expression during embryogenesis."
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY271746; AAP22958.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match 70.1%; Score 2562; DB 13; Length 678;
 Best Local Similarity 71.9%; Pred. No. 1.5e-146;
 Matches 498; Conservative 78; Mismatches 95; Indels 22; Gaps 11;

Qy	5	LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGKTCTCID	64
		: : : : : : : : : : : :	
Db	6	LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPPDSGSKSCIG	65
Qy	65	TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVGEFVS	124
		: : : : :	
Db	66	NKEGILQYCQEVYPELQITNVVEANQPVSIIWDWCKKSRKQCRSHMHIVVPIYRCLVGEFVS	125
Qy	125	DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF	184
		: : : : : :	
Db	126	DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF	185
Qy	185	VCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD	244
		: : : : : : : :	
Db	186	VCCP-ADAGKESESAAVEEDDSVWVGAEADYTENSMTR--DAAAEPAV--LEDDEDAD	240
Qy	245	DEDDEDGD-EVEEEAEPEYEEATERTT-SIATTTTTTTSVEEVVRVPTTAASTPDAVDK	302
		: : : : : : : : : :	
Db	241	EEDEDEDGDRDEKIEEEEEERTQSTSAALTSTTTTTTTSVEEVVRVPTPSSSPDAVDR	300
Qy	303	YLETPGDENENAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHFQE	362
		: :	
Db	301	YLET PADENENAHFLKAKESLET KHRERMSQVMREWEAERQAKSLPRNDKKAVIQHFQE	360
Qy	363	KVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKY	422
		: : : : : : :	
Db	361	KVEALEQESASERQQLVETHMARVEALLNDRRLALESYLSALQADPPRPRHVFSLLKKY	420
Qy	423	VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEE	482
		: : ::	
Db	421	VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVADD	480
Qy	483	IQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSLDD	542

	: : : :	
Db	481 IQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFGF	536
Qy	543 LQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH	602
	: : : : :	
Db	537 IHP-ESFN----QPNTHNQVEPVDARVPDLDLATRPVSGL---KPDDIPELRMEAEERH	588
Qy	603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVVE	662
	: : : :	
Db	589 S---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLVMLRKKQYTSIHGGIIE	645
Qy	663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	646 VDAAVTPEERHLSKMOONGYENPTYKFFEOMHN	678

Q90W28

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ID      Q90W28      PRELIMINARY;      PRT;      738 AA.
AC      Q90W28;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Amyloid precursor protein.
GN      APPA OR APP.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Groth C., Lardelli M.;
RT      "Expression analysis of zebrafish app.";
RL      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF389401; AAK64495.1; -.
DR      ZFIN; ZDB-GENE-000616-13; appa.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Protease inhibitor; Serine protease inhibitor.
SQ      SEQUENCE      738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

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Query Match 69.1%; Score 2524; DB 13; Length 738;
Best Local Similarity 66.3%; Pred. No. 3.2e-144;
Matches 500; Conservative 79; Mismatches 91; Indels 84; Gaps 14;

```
Qy      5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTCID 64
      | :||:| : |:||:| | ||||| |||||:| ||:|:| ||:| ||||:|:|
Db      6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPPSGSKSCIG 65

Qy     65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVGEFVS 124
      | ||||| ||||| ||||| ||||| |||||:| :||:| ||||:| | | :||| |||||
Db     66 NKEGILQYCQEVYPELQITNVVEANQPVSIIWDWCKKSRKQCRSHMHIVPIYRCLVGEFVS 125

Qy    125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
      | ||||| ||||| ||||| ||||| |||||:| ||:| ||||| |||||:| |||||
Db    126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy    185 VCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEEEEEADD 244
      |||| | : :|| | ||||| |||||:| || : | : : | | | :||:|:|
Db    186 VCCP-ADAGKESESAAVEEDSDVWVGAEADYTENSMT--DAAAPAVLE-DDEDADE 241

Qy    245 DED-DEGD-----EVEEEAEPEYEEATERTT-SIATTTTTTTESVEEVVR----- 288
      :|| |:|| :||| || || | : | : : :| ||||| |||||
Db    242 EEDEDQDGDGDRDEKIEEEEE--EERTQSTSAALTSTTTTTTTESVEEVREVCFASAET 299

Qy    289 -----VPTTAASTPDAVD 301
      :|| :|| |||||
Db    300 GPCRAMLRSWYYVREERRCAPFIYGGCGGNRNNFESEYCLSVCSGVLPTPSSSPDAVD 359

Qy    302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQ 361
      :||| ||||| ||||| || || ||||| ||||| |||||:| ||||| |||||
Db    360 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEAAERQAKSLPRNDKKAVIQHFQ 419

Qy    362 EKVESLEQEAAERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKK 421
      ||||:||||:|:||||| ||||| |||||:| ||||| |||||:| ||||| |||||:| |||
Db    420 EKVEALEQESASERQQLVETHMARVEALLNDRRLALESYLSALQADPPRPRHVSLLKK 479

Qy    422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVPAVAE 481
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    480 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIERMNSLGLLYKVPGVAD 539

Qy    482 EIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
      :|||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db    540 DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG 595

Qy    542 DLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR 601
      : | || || |:||||| || || || || || || || || || || || || || || ||
Db    596 FIHP-ESFN----QPNTHNQVEPVDARVPDLDLATRPVSGL---KPDDIPELRMEAEER 647

Qy    602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVV 661
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    648 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLVMLRKKQYTSIHGGII 704

Qy    662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    705 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 738
```

RESULT 12

Q8UUR9

ID Q8UUR9 PRELIMINARY; PRT; 694 AA.
AC Q8UUR9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative membrane protein.
GN APPB.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=11862463;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315639; CAC85736.1; -.
DR ZFIN; ZDB-GENE-020220-1; appb.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 694 AA; 79228 MW; 2B03382D411162DC CRC64;

Query Match 68.0%; Score 2482.5; DB 13; Length 694;
Best Local Similarity 67.7%; Pred. No. 9.5e-142;
Matches 476; Conservative 98; Mismatches 98; Indels 31; Gaps 9;

Qy 7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGKTCTIDTK 66
| | | : : | : | | | : | : | | | | : | | | : | | : | | : | | | |
Db 9 LLLMLTTLSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPTGTGKSCISTK 68
Qy 67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
| | | | : | | | | | : | | | | | | | | : | | | | : | | | : | | | | | | | |
Db 69 EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRQRCSHTHIVVPYRCLVGEFVSDA 128
Qy 127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
| | | | | | | | | | | | : | | : | | | | | | | : | : | | | | | | | | : | | | | | | | |
Db 129 LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC 188
Qy 187 CPLAEESDNVDSADAEEDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEEVEE 239
| | : | : | : | | : | | : | | | | | | : | | | : | | : | | : | |
Db 189 CPMEEQKD-LDSEEQEEANSVWWGGAETETDASVLKEQVTAKPDPVTEDEDLNNEE 247

[illegible]

09I9E7

DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;

Query Match 63.9%; Score 2334; DB 13; Length 612;
 Best Local Similarity 72.4%; Pred. No. 7.5e-133;
 Matches 459; Conservative 66; Mismatches 81; Indels 28; Gaps 12;

Qy	68	GILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDAL	127
Db	1	GILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVSDAL	60
Qy	128	LVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCC	187
Db	61	LVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVCC	120
Qy	188	PLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDED	247
		: : : : : : :	
Db	121	P-ADAGKESESAAVEEDSDVWVGGAADYTENSMTR--DAAAEPAV--LEDDEDADDEE	175
Qy	248	DEDGD-----EVEEEAEPEYEEATERTT-SIATTTTTTTESVEEVVRVPTTAASTPDAVD	301
		: : : : :	
Db	176	DEDGDGDRDEKIEEEEE--EERTQSTSAALTSTTTTTTESVDEVVRVPTPSSSPDAVD	233
Qy	302	KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHFQ	361
		:	
Db	234	RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEAEERQAKSLPRNDKKAVIQHFQ	293
Qy	362	EKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKK	421
		: : :	
Db	294	EKVEALEQESASERQQLVETHMARVEALLNDRRLALESYLSALQADPPRPRHVSLLKK	353
Qy	422	YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAE	481
Db	354	YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD	413
Qy	482	EIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD	541
		: :	
Db	414	DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG	469
Qy	542	DLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR	601
		:	
Db	470	FIHP-ESFN---QPNTHNQVEPVDPARVPDLATRPVSGL---KPDDIPELRMEAEER	521
Qy	602	HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGVV	661
		:	
Db	522	HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLVMLRKKQYTSIHGGII	578
Qy	662	EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	579	EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN	612

RESULT 14

Q8BPC7

ID Q8BPC7 PRELIMINARY; PRT; 384 AA.
 AC Q8BPC7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Amyloid beta (Fragment).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK076506; BAC36369.1; -.
 DR MGD; MGI:88059; App.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 52.6%; Score 1923; DB 11; Length 384;
 Best Local Similarity 97.9%; Pred. No. 2.8e-108;
 Matches 376; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 312 EHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEA 371
 |||
 Db 1 EHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEA 60
 Qy 372 ANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQ 431
 |||
 Db 61 ANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQ 120
 Qy 432 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEEIQDEVDELL 491
 |||
 Db 121 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEEIQDEVDELL 180
 Qy 492 QKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFLDDLPWHSFGA 551
 |||:|||||
 Db 181 QKEQNHSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFLDDLPWHPFGV 240
 Qy 552 DSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQ 611
 |||:|||||

Db	133	CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV	192
Qy	177	DKFRGVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAE	236
Db	193	DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD	245
Qy	237	VEE--EEA--DDDEDDDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTTESVE	284
Db	246	LEDFTAAVDEDEDEEEGEEVVEDRDYYYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT	303
Qy	285	EVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQ	344
Db	304	HDVKVPPTPLPTND--VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQ	362
Qy	345	AKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITA	404
Db	363	AKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAA	422
Qy	405	LQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE	464
Db	423	LQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEE	482
Qy	465	RMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTE	524
Db	483	RRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISE	525
Qy	525	TKTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGL-----	575
Db	526	TPVDVR--VSSEES-EEIPPFHPF--HPFPALPENEGSGVGEQ---DGGLIGAEKVIN	576
Qy	576	-TTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG	634
Db	577	SKNKVDENMVIDETLDVKEMIFNAE--RVGGLEERESVGPLREDFSLSSSALIGLLVIA	634
Qy	635	VVIATVIFITLVMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQ	694
Db	635	VAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYENPTYKYLEQMQ	694

Search completed: July 26, 2004, 12:46:36
Job time : 37.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 12:39:28 ; Search time 9 Seconds
(without alignments)
4032.544 Million cell updates/sec

Title: US-09-806-194A-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3585.5	98.2	770	1	A4_HUMAN	P05067 h amyloid b
2	3585.5	98.2	770	1	A4_MACFA	P53601 m amyloid b
3	3579	98.0	751	1	A4_SAISC	Q95241 s amyloid b
4	3530.5	96.6	770	1	A4_PIG	P79307 s amyloid b
5	3517.5	96.3	770	1	A4_CAVPO	Q60495 c amyloid b
6	3488.5	95.5	770	1	A4_MOUSE	P12023 m amyloid b
7	3488.5	95.5	770	1	A4_RAT	P08592 r amyloid b
8	2568	70.3	780	1	A4_TETFL	O73683 tetraodon f
9	2443.5	66.9	737	1	A4_FUGRU	O93279 fugu rubrip
10	1730	47.4	695	1	APP2_MOUSE	Q06335 mus musculu
11	1723	47.2	763	1	APP2_HUMAN	Q06481 homo sapien
12	1711	46.8	765	1	APP2_RAT	P15943 rattus norv
13	1185	32.4	650	1	APP1_HUMAN	P51693 homo sapien
14	1180	32.3	653	1	APP1_MOUSE	Q03157 mus musculu
15	816.5	22.4	686	1	A4_CAEEL	Q10651 caenorhabdi
16	755.5	20.7	887	1	A4_DROME	P14599 drosophila
17	287	7.9	59	1	A4_BOVIN	Q28053 bos taurus

18	283	7.7	58	1	A4_RABIT	Q28748	oryctolagus
19	283	7.7	58	1	A4_SHEEP	Q28757	ovis aries
20	282	7.7	58	1	A4_CANFA	Q28280	canis famil
21	278	7.6	57	1	A4_URSMA	Q29149	ursus marit
22	185.5	5.1	407	1	IE68_HSVSA	Q01042	herpesvirus
23	180.5	4.9	993	1	SCP1_MOUSE	Q62209	mus musculu
24	176	4.8	2004	1	MYS3_HUMAN	Q92794	homo sapien
25	175.5	4.8	802	1	NAB3_YEAST	P38996	saccharomyc
26	173.5	4.7	793	1	CALD_HUMAN	Q05682	homo sapien
27	172	4.7	771	1	CALD_CHICK	P12957	gallus gall
28	172	4.7	1498	1	GOA3_HUMAN	Q08378	homo sapien
29	169.5	4.6	297	1	TRT2_HUMAN	P45379	homo sapien
30	169.5	4.6	721	1	YCF2_OENPI	P31568	oenothera p
31	168.5	4.6	1875	1	MLP1_YEAST	Q02455	saccharomyc
32	168	4.6	1240	1	YNJ1_YEAST	P53935	saccharomyc
33	167.5	4.6	1976	1	MYHA_HUMAN	P35580	homo sapien
34	166.5	4.6	816	1	YG3A_YEAST	P53278	saccharomyc
35	166.5	4.6	1976	1	MYHA_RAT	Q9jlt0	rattus norv
36	164.5	4.5	1447	1	GOA3_MOUSE	P55937	mus musculu
37	163.5	4.5	681	1	MP10_HUMAN	O00566	homo sapien
38	162.5	4.4	712	1	NUCL_RAT	P13383	rattus norv
39	162	4.4	2017	1	MYSN_DROME	Q99323	drosophila
40	160.5	4.4	1976	1	MYHA_BOVIN	Q27991	bos taurus
41	160	4.4	694	1	NUCL_CHICK	P15771	gallus gall
42	159.5	4.4	1955	1	PUMA_PARUN	O61308	parascaris
43	158	4.3	301	1	TRT2_CHICK	P02642	gallus gall
44	157.5	4.3	706	1	NUCL_HUMAN	P19338	homo sapien
45	156.5	4.3	5596	1	MDN1_HUMAN	Q9nu22	homo sapien

ALIGNMENTS

RESULT 1

A4_HUMAN

ID A4_HUMAN STANDARD; PRT; 770 AA.

AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;

AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease

DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease

DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-

DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42

DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);

DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)

DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-

DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)

DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)

DE (Amyloid intracellular domain 50) (AID(50)); C31].

GN APP OR A4 OR AD1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]

RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM APP639).

RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [14]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [15]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [16]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [17]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [18]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [19]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [20]
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
 RP AND AD GLY-717.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 RN [21]
 RP SEQUENCE OF 656-737 FROM N.A.

RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 1.4e-168;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

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Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAAEPYEEATERTTSIATTTTTTTESVEEVVR----- 288
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Db    241 EADDDDEDDEDGDEVEEEAAEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    289 ----- 288
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Qy    289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 345
      :|||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 405
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

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Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    466 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 525
      |||
Db    541 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600

Qy    526 KTTVELLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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Db    601 KTTVELLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
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Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAIVIVITL 720
Qy      646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 2

A4_MACFA

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ID      A4_MACFA          STANDARD;          PRT;          770 AA.
AC      P53601; Q95KN7;
DT      01-OCT-1996 (Rel. 34, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
GN      APP.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC      TISSUE=Cerebellum;
RX      MEDLINE=91273117; PubMed=1905108;
RA      Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT      "Homology of the amyloid beta protein precursor in monkey and human
RT      supports a primate model for beta amyloidosis in Alzheimer's
RT      disease.";
RL      Am. J. Pathol. 138:1423-1435(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in
CC      cell mobility and transcription regulation through protein-protein
CC      interactions (By similarity). Can promote transcription activation
CC      through binding to APBB1/Tip60 and inhibit Notch signaling through
CC      interaction with Numb (By similarity). Couples to apoptosis-
CC      inducing pathways such as those mediated by G(0) and JIP (By
CC      similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC      Acts as a kinesin I membrane receptor, mediating the axonal
CC      transport of beta-secretase and presenilin 1 (By similarity). May
CC      be involved in copper homeostasis/oxidative stress through copper
CC      ion reduction. In vitro, copper-metallated APP induces neuronal
CC      death directly or is potentiated through Cu(II)-mediated low-
CC      density lipoprotein oxidation (By similarity). Can regulate
CC      neurite outgrowth through binding to components of the
CC      extracellular matrix such as heparin and collagen I and IV (By
CC      similarity). The splice isoforms that contain the BPTI domain
CC      possess protease inhibitor activity (By similarity).
CC      -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

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CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; M58727; AAA36829.1; -.
 DR EMBL; M58726; AAA36828.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(42) (POTENTIAL).

FT	CHAIN	688	711	P3(40) (POTENTIAL).
FT	CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT	CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT	CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT	CHAIN	740	770	C31 (POTENTIAL).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	724	734	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	739	740	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
 Best Local Similarity 90.0%; Pred. No. 1.4e-168;
 Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

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      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVEVEEE 240
Qy      241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVR----- 288
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEAETGPC 300
Qy      289 ----- 288
Db      301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLRKTTREPLTRD 360
Qy      289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 345
      :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
Qy      346 KNLPKADKKAVIQHFQEKVESLEQEAAERQQLVETHMARVEAMLNDRRLALENYITAL 405
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAAERQQLVETHMARVEAMLNDRRLALENYITAL 480
Qy      406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 525
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
Qy      526 KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 585
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 3

A4_SAISC

ID A4_SAISC STANDARD; PRT; 751 AA.

AC Q95241;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].

GN APP.

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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DR EMBL; S81024; AAD14347.1; -.
 DR HSSP; P05067; 1AAP.

DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 653 751 C99 (POTENTIAL).
 FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 669 751 C83 (POTENTIAL).
 FT CHAIN 669 694 P3(42) (POTENTIAL).
 FT CHAIN 669 692 P3(40) (POTENTIAL).
 FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).
 FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).
 FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).
 FT CHAIN 721 751 C31 (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 713 732 INTERACTION WITH G(O)-ALPHA
 FT (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION
 FT (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT SITE 652 653 CLEAVAGE (BY BETA-SECRETASE)
 FT (BY SIMILARITY).
 FT SITE 653 654 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 668 669 CLEAVAGE (BY ALPHA-SECRETASE)
 FT (BY SIMILARITY).
 FT SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION
 FT (BY SIMILARITY).

FT	SITE	687	687	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT	SITE	692	693	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT	SITE	694	695	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9) (BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL.
FT	SITE	740	743	NPXY MOTIF.

Query Match 98.0%; Score 3579; DB 1; Length 751;
Best Local Similarity 91.9%; Pred. No. 2.9e-168;
Matches 690; Conservative 2; Mismatches 3; Indels 56; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG <td>60</td>	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVR-----	288
Db	241	EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	289	-----VPTTAASTPDAVDKYL	304
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVIPTTAASTPDAVDKYL	360
Qy	305	ETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKV	364
Db	361	ETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKV	420
Qy	365	ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR	424
Db	421	ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR	480
Qy	425	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ	484
Db	481	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ	540
Qy	485	DEVDELLQKEQNYSDDLNMI SEPRISYGNDALMPSLTETKTTVELLPVNGEFLDDDLQ	544

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Db      541 DEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600
Qy      545 PWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 604
        |||
Db      601 PWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 660
Qy      605 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGVEVD 664
        |||
Db      661 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVD 720
Qy      665 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
        |||
Db      721 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751

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RESULT 4

A4_PIG

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ID      A4_PIG          STANDARD;          PRT;    770 AA.
AC      P79307; Q29023; Q9TUI0;
DT      01-NOV-1997 (Rel. 35, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kimura A., Takahashi T.;
RT      "Amyloid precursor protein 770.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE OF 1-136 FROM N.A.
RC      TISSUE=Small intestine;
RA      Winteroe A.K., Fredholm M.;
RT      "Evaluation and characterization of a porcine small intestine cDNA
RT      library.";
RL      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE OF 667-723 FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in

```

cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(O) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction (By similarity). In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity).

-!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

-!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

-!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the

CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).

CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).

CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC -----

DR EMBL; AB032550; BAA84580.1; -.

DR EMBL; Z84022; CAB06313.1; -.

DR EMBL; X56127; CAA39592.1; -.

DR HSSP; P05067; 1AAP.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;

KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;

KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;


```

Db      61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120
Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        |||:|||||:|||||
Db      181 GVEFVCCPLAEESDNIDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240
Qy      241 EADDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVR----- 288
        ||:|||||
Db      241 EAEDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
Qy      289 ----- 288
Db      301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLLKTTQEHL PQD 360
Qy      289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 345
        :|||||
Db      361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
Qy      346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
        |||
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
Qy      406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
        |||
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 525
        |||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Qy      526 KTTVELLPVNGEFLDDLPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 585
        |||
Db      601 KTTVELLPVNGEFLDDLPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      586 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
        |||
Db      661 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
        |||
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770

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RESULT 5

A4_CAVPO

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ID      A4_CAVPO          STANDARD;          PRT;    770 AA.
AC      Q60495; Q60496;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid

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DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN APP.
OS *Cavia porcellus* (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; *Cavia*.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Liver;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
RN [2]
RP INTERACTION OF BETA-APP40 WITH APOE.
RX MEDLINE=98007700; PubMed=9349544;
RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT cerebral capillary sequestration and blood-brain barrier transport of
RT circulating Alzheimer's amyloid beta.";
RL J. Neurochem. 69:1995-2004(1997).
RN [3]
RP PROCESSING.
RX MEDLINE=20084499; PubMed=10619481;
RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.;
RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.";
RL Neuroscience 95:243-254(2000).
RN [4]
RP GAMMA-SECRETASE PROCESSING.
RX MEDLINE=20576391; PubMed=11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RT "A novel gamma -secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor.";
RL J. Biol. Chem. 276:481-487(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(0) and JIP (By
CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metallated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can

CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins E and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC ApoE3 appears to be the preferred amyloid binding isoform, while
 CC the apoE4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -!- INDUCTION: Increased levels during neuronal differentiation.
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of

CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.

CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).

CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).

CC -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the appicans (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.

CC -!- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----

DR EMBL; X97631; CAA66230.1; -.
 DR EMBL; X99198; CAA67589.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.

Qy 406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
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 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
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 Qy 466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 525
 |||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
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 Qy 526 KTTVELLPVNGEFLDDLQPWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
 |||
 Db 601 KTTVELLPVNGEFLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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 Qy 586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
 |||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Qy 646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
 |||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
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RESULT 6

A4_MOUSE

ID A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023; P97487; P97942; Q99K32;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
 DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 DE 50) (AID(50)); C31].
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [2]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RA Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN [5]

RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

RN [8]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of *Mus domesticus*.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Mengod G., Ghatti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-I.";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.
 RX MEDLINE=22008109; PubMed=12011466;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid

RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RT nuclear fraction of neurones in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(0) and JIP. Inhibits G(0) alpha ATPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
 CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.5%; Score 3488.5; DB 1; Length 770;
 Best Local Similarity 87.7%; Pred. No. 8.1e-164;
 Matches 675; Conservative 6; Mismatches 14; Indels 75; Gaps 1;

AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
 DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
 DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
 DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
 DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
 DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 RN [3]
 RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
 RX MEDLINE=21443797; PubMed=11483588;
 RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 RT family resembling gamma-secretase-like cleavage of Notch.";
 RL J. Biol. Chem. 276:35235-35238(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 RT isoforms.";
 RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
 RN [5]
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=95263526; PubMed=7744833;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
 RA Mytilineou C., Margolis R.U., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 RT brain and is produced by astrocytes but not by neurons in primary
 RT neural cultures.";
 RL J. Biol. Chem. 270:11839-11844(1995).
 RN [6]
 RP TISSUE SPECIFICITY OF ISOFORMS.

RX MEDLINE=97150061; PubMed=8996834;
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 RT and aging.";
 RL Gerontology 43:119-131(1997).
 RN [7]
 RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
 RP TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
 RT Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556(1999).
 RN [8]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024358;
 RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouilliot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Go heterotrimeric
 RT protein within a cell compartment specialized in signal
 RT transduction.";
 RL J. Neurosci. 19:1717-1727(1999).
 RN [9]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970;
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 RT splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10388-10391(1995).
 RN [10]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
 RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 RT peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616(1999).
 RN [11]
 RP BETA-AMYLOID ZINC BINDING.
 RX MEDLINE=99343552; PubMed=10413512;
 RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 RT of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX MEDLINE=21956095; PubMed=11959460;
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;

RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX MEDLINE=99262094; PubMed=10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate E in the repeating disaccharide region
 RT and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
 CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 95.5%; Score 3488.5; DB 1; Length 770;
 Best Local Similarity 87.5%; Pred. No. 8.1e-164;
 Matches 674; Conservative 8; Mismatches 13; Indels 75; Gaps 1;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
 ||| ||||||||| |||||||||||||||||||||:|||||||:|||||
 Db 1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
 ||| ||||||||||||||||||||||||||||||||||| | |||||||
 Db 61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPIYRCLVG 120
 Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 |||||||||||||||||||||||||||||||||||||||||||||
 Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 Qy 181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
 |||||||||||||:||||||||||||||||||| |||||||||:|||||
 Db 181 GVEFVCCPLAEESDSIDSADAEEEDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEEE 240
 Qy 241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVR----- 288
 ||:|||| |||||||||||||||||||||||||||||||||
 Db 241 EAEDDEDVEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
 Qy 289 ----- 288
 Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSVSSQSLKTTSEPLPQD 360

Qy 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
:|||||
Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy 346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITAL 405
|||||
Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITAL 480

Qy 406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
|||||
Db 481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTET 525
|||||
Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTET 600

Qy 526 KTTVELLPVNGEFSDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 585
|||||
Db 601 KTTVELLPVNGEFSDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
|||||
Db 661 IKTEEISEVKMDAEFGHDSGFVHRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 695
|||||
Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770

RESULT 8

A4_TETFL

ID A4_TETFL STANDARD; PRT; 780 AA.
AC O73683;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252138; PubMed=9599080;
RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL Gene 210:17-24(1998).
CC !- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- SIMILARITY: Belongs to the APP family.
CC !- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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DR EMBL; AF018165; AAC41275.1; -.
 DR HSSP; P05067; 1HZ3.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT CHAIN 682 724 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 19 711 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 712 732 POTENTIAL.
 FT DOMAIN 733 780 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 323 382 BPTI/KUNITZ INHIBITOR.
 FT SITE 769 772 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 327 378 BY SIMILARITY.
 FT DISULFID 336 361 BY SIMILARITY.
 FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 70.3%; Score 2568; DB 1; Length 780;
 Best Local Similarity 65.3%; Pred. No. 9.3e-119;
 Matches 512; Conservative 71; Mismatches 95; Indels 106; Gaps 10;

Qy 7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTIDTK 66
 |||:| : | |||| : |||||:||||:| : ||||:| : ||||:| ||
 Db 8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPPDSGKTSCIGTK 67
 Qy 67 EGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
 |||||:|||||:|||||:||||:| | :|:|||||:|||||
 Db 68 EGILQYCQEVYPQLQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127
 Qy 127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
 |||||:|||||:|||||:| :: |||||:|||||

Db 128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC 187

Qy 187 CPLAEESDNVDSADAEEDSDVWVGADTDYADGS-----EDKVVEVAEEE 232
 || || :|| : : ||||| ||||| ||:| | ||| ||

Db 188 CP-AEAERDMDSTEKDADSDVWVGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEG 246

Qy 233 EVAEVEEEE-----ADDEDEDGDEVEEEAEEPVEEATERTTSIA 273
 |||: :|| | |||: ||| ||: | :| | ||:|

Db 247 EVAQEDDEEEELDTDQDGDGEEDHEAADDEEEEDVDEIDAFGESDDVDADEPTTNVA 306

Qy 274 ---TTTTTTTSEVEEVVR----- 288
 ||||| |||||

Db 307 MTTTTTTTTTSEVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGNMN 366

Qy 289 -----VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ 333
 || | :||| ||| ||||| ||||| ||||| |||||

Db 367 NFEESEYCLSVCSVVPTDMPSSPDAVDHYLETADENEHAHFQAKESLEAKHRERMSQ 426

Qy 334 VMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 393
 ||||| :||| || | ||||: ||||: ||||| :|||

Db 427 VMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEALLNDR 486

Qy 394 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVPDKKAAQIRS 453
 ||||| :||| ||||| :||||| ||||| ||||| |||||

Db 487 RRLALENYLTALQQDPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVPDKKAAQIRP 546

Qy 454 QVMTHLRVIYERMNQSLSLLYNPAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISY 513
 ||: |||| | |||| || | ||: ||: | |||: | |||: :| :||

Db 547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVVRVSY 605

Qy 514 GNDALMPSLTETKTTVELLPVNGEFLDDLQPDWH--SFGADSVPAANTENEVEPVDARPA 571
 ||||| :|| | :| : | | ||||| :|||

Db 606 GNDALMPDQELGDGQADLLP--QEDTLGGVGVFHPESFN----QLNTENQVEPVD SRPTF 659

Qy 572 DRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAI IGLM 631
 :||: ||| :| | : ||: || | : ||||| ||||| ||||| |||||

Db 660 ERGVPTRP--VTGKSMEAVPEL RMETEDRQSTEYEVHHQKL VFFAEDVGSNKGAI IGLM 716

Qy 632 VGGVVIATVIFITLVMLKKKQYTSIHGHVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
 ||||| ||||| :||||| :||||| ||||| ||||| ||||| |||||

Db 717 VGGVVIATVIVITLVMLRKKQYTSIHGHIIEVDAAVTPEERHLSKMQQNGYENPTYKFFE 776

Qy 692 QMQN 695
 ||||

Db 777 QMQN 780

RESULT 9

A4_FUGRU

ID A4_FUGRU STANDARD; PRT; 737 AA.

AC 093279;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.

```

OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL          1      18      POTENTIAL.
FT   CHAIN           19     737     ALZHEIMER'S DISEASE AMYLOID A4
FT                                     PROTEIN HOMOLOG.
FT   CHAIN           639     681     BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN          19     668     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        669     689     POTENTIAL.
FT   DOMAIN          690     737     CYTOPLASMIC (POTENTIAL).
FT   DOMAIN          286     344     BPTI/KUNITZ INHIBITOR.
FT   SITE            726     729     CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE        300     301     REACTIVE BOND.

```


Qy 663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
 |||||:|||||
 Db 705 VDAAVTPEERHLARMQQNGYENPTYKFFEQMQN 737

RESULT 10

APP2_MOUSE

ID APP2_MOUSE STANDARD; PRT; 695 AA.
 AC Q06335;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
 GN APLP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RA von der Kammer H.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 1-246 FROM N.A.
 RX MEDLINE=94032480; PubMed=8218408;
 RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
 RT "The complete cDNA coding sequence for the mouse CDEI binding
 RT protein.";
 RL Biochim. Biophys. Acta 1216:154-156(1993).
 RN [3]
 RP SEQUENCE OF 185-695 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RX MEDLINE=93129193; PubMed=1482349;
 RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
 RT "A murine sequence-specific DNA binding protein shows extensive local
 RT similarities to the amyloid precursor protein.";
 RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
 RN [4]
 RP SEQUENCE OF 1-35 FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=96029629; PubMed=7592716;
 RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
 RT "The mouse APLP2 gene. Chromosomal localization and promoter
 RT characterization.";
 RL J. Biol. Chem. 270:25475-25480(1995).
 CC -!- FUNCTION: Binds to the DNA 5'-GTCACATG-3' (CDEI box) which plays
 CC an important role in the early development of embryos.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -----
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CC -----
 DR EMBL; Z22592; CAA80306.1; -.
 DR EMBL; M97216; AAA20039.1; -.
 DR EMBL; U34291; AAC52318.1; -.
 DR PIR; JC1404; JC1404.
 DR PIR; S38344; S38344.
 DR HSSP; P05067; 1MWP.
 DR MGD; MGI:88047; Aplp2.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Transmembrane; DNA-binding; Signal; Nuclear protein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 625 648 POTENTIAL.
 FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 218 231 POLY-GLU.
 FT DOMAIN 256 266 POLY-GLU.
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 185 189 GMLLP -> MACCC (IN REF. 3).
 SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 47.4%; Score 1730; DB 1; Length 695;
 Best Local Similarity 49.2%; Pred. No. 8.3e-78;
 Matches 359; Conservative 118; Mismatches 163; Indels 90; Gaps 19;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
 | :||| || | : ||| :||||| ||:||||:|:| |||: ||
 Db 15 LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPPD 74
 Qy 57 SGTKTCTIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 :|||:|: ||| :|||||:|||||||:||||| | :||:| :|||: | |||:|
 Db 75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132
 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGI 176
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 Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLP CGV 192
 Qy 177 DKFRGVEFVCCPLAE--ESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEVAE---E 231
 |:| | |:||| : :||: | : ||:| | | || : :| |
 Db 193 DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLDKSEFPTE 243
 Qy 232 EEVAEVEVEEAD-DEDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTTES 282
 :: : | || :||:|:|:| | : : | | | | : : | : :
 Db 244 ADLEDFTAAADEEEDEEEGEEVVEDRDYYDPFKGDDYNE--ENPTSPSSEGTISDK 301
 Qy 283 VEEVVRVPTTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 342

[illegible]

RC TISSUE=Ovary;
 RX MEDLINE=95217334; PubMed=7702756;
 RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
 RT "A human amyloid precursor-like protein is highly homologous to a
 RT mouse sequence-specific DNA-binding protein.";
 RL DNA Cell Biol. 13:1137-1143(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94035131; PubMed=8220435;
 RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
 RA Hyman B.T., Neve R.L., Tanzi R.E.;
 RT "Isolation and characterization of APLP2 encoding a homologue of the
 RT Alzheimer's associated amyloid beta protein precursor.";
 RL Nat. Genet. 5:95-99(1993).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May play a role in the regulation of hemostasis. The
 CC soluble form may have inhibitory properties towards coagulation
 CC factors. May interact with cellular G-protein signaling pathways.
 CC May bind to the DNA 5'-GTACATG-3'(CDEI box).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q06481-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q06481-2; Sequence=VSP_000018;
 CC Name=3;
 CC IsoId=Q06481-3; Sequence=VSP_000019;
 CC -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney
 CC and endothelial tissues.
 CC -!- SIMILARITY: Belongs to the APP family.

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CC      -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; S60099; AAC60589.1; -.
DR      EMBL; L09209; AAA35526.1; -.
DR      EMBL; Z22572; CAA80295.1; -.
DR      EMBL; L27631; AAC41701.1; -.
DR      EMBL; BC000373; AAH00373.1; -.
DR      PIR; A49321; A49321.
DR      HSSP; P05067; 1MWP.
DR      Genew; HGNC:598; APLP2.
DR      MIM; 104776; -.
DR      GO; GO:0016021; C:integral to membrane; NAS.
DR      GO; GO:0005634; C:nucleus; IDA.
DR      GO; GO:0003677; F:DNA binding; NAS.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Transmembrane; Signal; Alternative splicing; DNA-binding;
KW      Nuclear protein; Serine protease inhibitor.
FT      SIGNAL          1          29          POTENTIAL.
FT      CHAIN           30         763          AMYLOID-LIKE PROTEIN 2.
FT      DOMAIN          30         692          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        693         716          POTENTIAL.
FT      DOMAIN          717         763          CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          215         280          ASP/GLU-RICH (HIGHLY ACIDIC).
FT      DOMAIN          306         364          BPTI/KUNITZ INHIBITOR.
FT      DOMAIN          215         231          POLY-GLU.
FT      ACT_SITE        320         321          REACTIVE BOND (BY SIMILARITY).
FT      DISULFID        310         360          BY SIMILARITY.
FT      DISULFID        319         343          BY SIMILARITY.
FT      DISULFID        335         356          BY SIMILARITY.
FT      VARSPLIC        308         363          Missing (in isoform 2).
FT                                     /FTId=VSP_000018.
FT      VARSPLIC        613         624          Missing (in isoform 3).
FT                                     /FTId=VSP_000019.
FT      CONFLICT        543         543          S -> I (IN REF. 1).
SQ      SEQUENCE       763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

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Query Match 47.2%; Score 1723; DB 1; Length 763;
Best Local Similarity 47.0%; Pred. No. 2e-77;
Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;

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Db     15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy     57 SGTKTCTIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
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Db     75 TGTKSCFETKEEVLYCQEQEMYPELQITNVMEANQVRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy    117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
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Db    133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy    177 DKFRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAE 236
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Db    193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD 245

Qy    237 VEE--EEA--DDDEDDDEDGDEVEEEAEOPY-----EEATERTTSIATTTTTTTES 282
      : | : | | : | | | : | | | : | | | : | | | : | | | : | | |
Db    246 LEDFTEAAVDEDEDEEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy    283 VEEV-----VRVP 290
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Db    306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGCGGNRNNFESDYCMVCKAMIP 365

Qy    291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
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Db    366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy    351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPP 410
      | : : : | | | | | : | | | : | | | : | | | : | | | : | | | : | |
Db    425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy    411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
      | | : | : | | | | | | | | | : | | | : | | | : | | | : | | |
Db    485 RPHRILQALRRYVRAENKDRDLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERNQSL 544

Qy    471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTIVE 530
      | | | | | | | | | : | | | : | | | : | | | : | | | : | | |
Db    545 SLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISETPVDVR 587

Qy    531 LLPVNGEFSDDLQPVWSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN----- 585
      | : | | : : | : | | | | | | | | | | | | | | | | | | | |
Db    588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGG 635

Qy    586 IKTEE---ISEVKMDAEFRHDSGYEVHQQKLVFFAEDVGS-----NKG 625
      | | | | | : | : | | | : | : : : | | | | | | | | | | |
Db    636 IGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEERESVGPLREDFSLSS 693

Qy    626 AIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGHVVEVDAAVTPEERHLSKMQQNGYENP 685
      | : | | | : | | | | | : | | | : | | | : | | | : | | | : | | |
Db    694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYENP 753
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Qy 686 TYKFFEQMQ 694
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 Db 754 TYKYLEQMQ 762

RESULT 12

APP2_RAT

ID APP2_RAT STANDARD; PRT; 765 AA.
 AC P15943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
 GN APLP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-627 FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain, and Heart;
 RX MEDLINE=94368849; PubMed=8086458;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
 RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
 RT difference to human and murine homologues."
 RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A;
 CC IsoId=P15943-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P15943-2; Sequence=VSP_000021;
 CC Name=C;
 CC IsoId=P15943-3; Sequence=VSP_000020;
 CC Name=D;
 CC IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
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DR EMBL; X77934; CAA54906.1; -.
 DR EMBL; M31322; AAA42352.1; -.
 DR PIR; A35981; A35981.
 DR PIR; S42880; S42880.
 DR HSSP; P05067; 1MWP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
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 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;
 KW Signal; Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 696 718 POTENTIAL.
 FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 322 323 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 312 362 BY SIMILARITY.
 FT DISULFID 321 345 BY SIMILARITY.
 FT DISULFID 337 358 BY SIMILARITY.
 FT DOMAIN 218 229 POLY-GLU.
 FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT VARSPLIC 311 365 Missing (in isoform C and isoform D).
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 FT CONFLICT 575 577 DQF -> EFV (IN REF. 2).
 SQ SEQUENCE 765 AA; 86882 MW; CF51FCCCE305A0CF CRC64;

Query Match 46.8%; Score 1711; DB 1; Length 765;
 Best Local Similarity 46.1%; Pred. No. 7.9e-77;
 Matches 363; Conservative 122; Mismatches 167; Indels 136; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
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 Db 15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74
 Qy 57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
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 Db 75 TGTKSCLGTKEEVLYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132
 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
 ||||| |||: |:| ||||:||| | ||| || | : |: |||||:
 Db 133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98088960; PubMed=9428684;
 RA Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
 RA Masters C.L., Beyreuther K., Weidemann A.;
 RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
 RT expression in COS-7 cells and identification of soluble forms in the
 RT cerebrospinal fluid.";
 RL Eur. J. Biochem. 250:354-363(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98180887; PubMed=9521588;
 RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
 RA Olsen A., Tryggvason K.;
 RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
 RT 19q13.1.";
 RL Hum. Genet. 102:192-196(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=96115107; PubMed=7494461;
 RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
 RA Black I.B.;
 RT "Selective localization of amyloid precursor-like protein 1 in the
 RT cerebral cortex postsynaptic density.";
 RL Brain Res. Mol. Brain Res. 32:36-44(1995).
 RN [5]
 RP HEPARIN AND ZINC BINDING.
 RX MEDLINE=95014513; PubMed=7929392;
 RA Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
 RT "The amyloid beta-protein precursor and its mammalian homologues.
 RT Evidence for a zinc-modulated heparin-binding superfamily.";
 RL J. Biol. Chem. 269:26618-26621(1994).

RN [6]
RP INTERACTION WITH APBA2.
RX MEDLINE=99107877; PubMed=9890987;
RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA Sakiyama S., Kirino Y., Suzuki T.;
RT "Interaction of a neuron-specific protein containing PDZ domains with
RT Alzheimer's amyloid precursor protein.";
RL J. Biol. Chem. 274:2243-2254(1999).

RN [7]
RP EXTRACELLULAR COPPER-BINDING.
RX MEDLINE=22130992; PubMed=12135352;
RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
RA Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA Bayer T.A., Multhaup G.;
RT "Evidence for a copper-binding superfamily of the amyloid precursor
RT protein.";
RL Biochemistry 41:9310-9320(2000).

CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALID1, activates transcription
CC activation through APBB1 (Fe65) binding (By similarity). Couples
CC to JIP signal transduction through C-terminal binding. May
CC interact with cellular G-protein signaling pathways. Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I.
CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APBA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC localized to the postsynaptic density (PSD).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.
CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC similarity).
CC -!- PTM: N- and O-glycosylated.
CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -!- SIMILARITY: Belongs to the APP family.

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CC -----

DR EMBL; U48437; AAB96331.1; -.
 DR EMBL; AD000864; AAB50173.1; -.
 DR EMBL; BC012889; AAH12889.1; -.
 DR HSSP; P05067; 1MWP.
 DR Genew; HGNC:597; APLP1.
 DR MIM; 104775; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 650 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 621 650 C30 (BY SIMILARITY).
 FT DOMAIN 39 580 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 581 603 POTENTIAL.
 FT DOMAIN 604 650 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 178 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 204 211 ZINC-BINDING.
 FT DOMAIN 310 342 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 410 441 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 442 459 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 640 643 CLATHRIN-BINDING (POTENTIAL).
 FT DOMAIN 241 247 POLY-GLU.
 FT DOMAIN 264 268 POLY-GLU.
 FT SITE 167 167 REQUIRED FOR COPPER(II) REDUCTION (BY
 FT SIMILARITY).
 FT SITE 604 615 BASOLATERAL SORTING SIGNAL (BY
 FT SIMILARITY).
 FT SITE 620 621 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
 FT SITE 638 641 ENDOCYTOSIS SIGNAL (BY SIMILARITY).
 FT SITE 640 643 NPXY MOTIF.
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 48 48 A -> P (IN REF. 1).
 SQ SEQUENCE 650 AA; 72176 MW; B95F0F4D1C5CBAC7 CRC64;

Query Match 32.4%; Score 1185; DB 1; Length 650;
 Best Local Similarity 38.7%; Pred. No. 3.6e-51;
 Matches 271; Conservative 115; Mismatches 231; Indels 84; Gaps 16;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHNMVQNGKWDSDPSGTK 60
 :|| | ||| | :| : | | | :| ||| :| :: |:| :| :| :|
 Db 23 LLPLLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCLV 119
 |: : :|:|:|:|:|:| | :| | : :| | | | | |:|:|:|:|
 Db 83 RCLRDPQRVLEYCRQMPYELQIARVEQATQAIPIMERWCGGSRSGSCAHPHHQVVPFRCLP 142

Qy 120 GEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF 179
 |||||:|||||: |:||||||| ||: | |:| || : || ||||| |:|
 Db 143 GEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGLMPCGSDRF 202
 Qy 180 RGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 239
 ||||:|||| | | | | | | | | | | | | | | | | | |
 Db 203 RGVEYVCCPPPGTPD--PSGTAVGDPSTRSW-----PPGSR---VEGADEEE----EE 246
 Qy 240 EEADDDDEDD--EDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTP 297
 | | | | : : ||| | | : | : | | | | | | | | | |
 Db 247 ESFPQPVDYFVEPPQAE--EETVPPSSHTLAVVGKVTPTPR-----PT----- 291
 Qy 298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVI 357
 | | | | ||: :|| | :|| | | : :||| | | | | | | | | | |
 Db 292 DGVDIYFGMPGEI SEHEGFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALN 351
 Qy 358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN 417
 :||| :|||: : |||:|||| | | | :||| | | | : ||| | | : |
 Db 352 EHFQSIQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQADPPQAERVLL 411
 Qy 418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
 | :| :| | | | :| :| | | | | | | | | | | | | | | | | | |
 Db 412 ALRRYLRAEQKEQRHTLRHYQHVAVDPEKAQQMRQVHTLQVIEERVNQSGLLDQNP 471
 Qy 478 AVAAEQDEVDLQKEQNYSDVLNMISEPRISYGNLMPSLTETKTTVELLPVNGE 537
 :| :| :| :| | | | | | | | | | | | | | | | | | |
 Db 472 HLAQELRPQIQELLHSEH-----LGPSELEA-----PAPGG 502
 Qy 538 FSLD--DLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVK 595
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 503 SSEDKGLQPPDS--KDDTPM-----TLPKGSTEQDAASPEKEKMNPLEQYE 547
 Qy 596 MDAEFRHDSGYEVHH--QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKK 651
 | : | | | : | : | | | : | : | : | : | : | : | : | | | | | |
 Db 548 RKNVASVPRGFPHSSEIQRDELAPAGTGVSRVAVSGLLIMAGGSLIVLSMLLLRRKK 607
 Qy 652 QYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQ 692
 | : | | | | | : | | | : | : | : | | | | | | | | | | | |
 Db 608 PYGAISHGVVEVDPMILTLEEQQLRELQRHGYENPTYRFL 648

RESULT 14

APP1_MOUSE

ID APP1_MOUSE STANDARD; PRT; 653 AA.
 AC Q03157; Q8VC38;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
 GN APLP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RX MEDLINE=93066322; PubMed=1279693;
 RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
 RA Solomon F.;
 RT "Identification of a mouse brain cDNA that encodes a protein related
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP COLLAGEN-BINDING.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RP INTERACTION WITH DAB1.
 RX MEDLINE=99389880; PubMed=10460257;
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1.";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RP INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
 RP TYR-641.

RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamio L.;
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RT secretase regulates transcription.";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, ALID1, activates transcription
 CC activation through APBB1 (Fe65) binding. Couples to JIP signal
 CC transduction through C-terminal binding. May interact with
 CC cellular G-protein signaling pathways. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB and APBA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N- and O-glycosylated.
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: Belongs to the APP family.

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DR EMBL; L04538; AAA37247.1; -.
 DR EMBL; BC021877; AAH21877.1; -.
 DR PIR; A46362; A46362.
 DR HSSP; P05067; 1MWP.
 DR MGD; MGI:88046; Aplp1.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;

KW	Glycoprotein.			
FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	653	AMYLOID-LIKE PROTEIN 1.
FT	CHAIN	624	653	C30 (BY SIMILARITY).
FT	DOMAIN	38	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	606	POTENTIAL.
FT	DOMAIN	607	653	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	157	177	COPPER-BINDING.
FT	DOMAIN	203	210	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	313	345	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	413	444	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	445	462	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	263	271	POLY-GLU.
FT	DOMAIN	535	538	POLY-SER.
FT	DOMAIN	601	606	POLY-LEU.
FT	SITE	166	166	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT	SITE	607	618	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	623	624	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	641	644	ENDOCYTOSIS SIGNAL.
FT	SITE	643	646	NPXY MOTIF.
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	554	554	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN	641	641	Y->G: REDUCED BINDING OF APBB1.
FT	CONFLICT	17	17	P -> PP (IN REF. 2).
SO	SEQUENCE	653 AA;	72750 MW;	56516DC3EA40E4B0 CRC64;

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      :|||  ::||:: : |||:||||  || |:|:|  |||  :: |||  ||:  |
Db      355 EHFQSIQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPOAERVLM 414
Qy      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
      |:|:|:|:|:|:|:|:|:|:|  |||:|  |:|  ||  |||:|  |||||  ||  |
Db      415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474
Qy      478 AVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
      |:|:|:|  :: |||  ||  :  :  ||  :|  |  :|  |
Db      475 HLAQELRPQIQELL-----LAEHLGPSEL----DASVPGSSSEDK----- 510
Qy      537 EFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
      |||  |:|  :|  |  :|  |  :  |  :  :  :
Db      511 ----GSLQP-----PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551
Qy      597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKKQ 652
      |:  |  |:  |  :|  |:|:|  |  :|  :|:|:|  |||
Db      552 KVNASAPRGFPFHSSDIQRDELAPSGTGVREALSGLLIMGAGGGS LIVLSLLLLRKKKP 611
Qy      653 YTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
      |:|  |||||  :|  ||:  |  :|:|:|:|:|:|  |:
Db      612 YGTISHGVVEVDPMLTLEEQLRELQRHGYENPTYRFL 651

```

RESULT 15

A4_CAEEL

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ID      A4_CAEEL          STANDARD;          PRT;      686 AA.
AC      Q10651; Q18583; Q95ZX1;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Beta-amyloid-like protein precursor.
GN      APL-1 OR C42D8.8.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE OF 6-686 FROM N.A.
RC      STRAIN=Bristol N2;
RX      MEDLINE=94089766; PubMed=8265668;
RA      Daigle I., Li C.;
RT      "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT      the human beta-amyloid protein precursor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049 (1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RA      Hallsworth K.;
RL      Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      REVISIONS, AND ALTERNATIVE SPLICING.
RA      Waterston R.;
RL      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;

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CC      Name=a;
CC      IsoId=Q10651-1; Sequence=Displayed;
CC      Name=b;
CC      IsoId=Q10651-2; Sequence=VSP_000017;
CC      Note=No experimental confirmation available;
CC      -!- SIMILARITY: Belongs to the APP family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U00240; AAC46470.1; ALT_INIT.
DR      EMBL; U56966; AAA98722.1; -.
DR      EMBL; U56966; AAK68242.1; -.
DR      PIR; T15795; T15795.
DR      HSSP; P05067; 1MWP.
DR      WormPep; C42D8.8a; CE04209.
DR      WormPep; C42D8.8b; CE27845.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
KW      Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW      Alternative splicing.
FT      SIGNAL      1      21      POTENTIAL.
FT      CHAIN      22      686      BETA-AMYLOID-LIKE PROTEIN.
FT      DOMAIN      22      621      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      622      642      POTENTIAL.
FT      DOMAIN      643      686      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      205      228      ASP-RICH.
FT      DOMAIN      676      679      CLATHRIN-BINDING (POTENTIAL).
FT      CARBOHYD      84      84      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      201      201      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      249      249      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      417      417      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC      538      539      Missing (in isoform b).
FT      /FTId=VSP_000017.
SQ      SEQUENCE      686 AA; 79434 MW; A0816858FDD48608 CRC64;

Query Match      22.4%; Score 816.5; DB 1; Length 686;
Best Local Similarity 29.1%; Pred. No. 4.2e-33;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60
      :: || : :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTTDDERYA 63

Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || | | | :|| : : || : ||| : || : | : || : || | | | | : |
Db      64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

```

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLP 174
 || :|| || :| | | : || | : | | : : :|| ||
 Db 123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy 175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEV 234
 :| | ||||| :| : | : :
 Db 183 ALDMFTGVEFVCCP----NDQTNKTDVQKTK----- 209

Qy 235 AEVEEEEADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
 |::| ||||| | : ||::| ||
 Db 210 ---EEDDDDDDEDDAYEDDYSEESDEKDEE----- 236

Qy 295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEA-----ERQAKNLP 349
 | : | | : ||| |::| : : ||::| : ||::| : | : ||: |
 Db 237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy 350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL- 405
 | :| | | ||: | ||:| |::| | ||:||||::| | :| ||
 Db 295 KGAEKFKSQMNARFQKTVSSLEEEHKMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy 406 -QAVPPRPRHVFNMMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLVIYE 464
 | | || |::|:|||| ||| : | : | |::| : | : || |
 Db 355 THVNKPNKHSVLQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy 465 RMNQSLSLLYNVP-----AVA--EEIQDEVDELLQKEQNYSDVLANMISEPRISY 513
 |:| :::| : | || : : ||| : | | | :| : |
 Db 415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE---DSELTPIIHDDFSK 470

Qy 514 GN--DALMPSLT----ETKTTVELLPVNGEFLDDLQPWHSFGADSVFANT---ENEVEP 564
 | | :| : : :|| | : : : | | : : :|
 Db 471 NAKLDVKAPTTTAKPVKETDNAKVLPTASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy 565 VДАРP-----AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
 || :| | | | | | : : :| | | : :|
 Db 531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDDSSSSTSSSEDEDEDKNIKELRVDI 590

Qy 599 E-----FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLK 649
 | :|| | :| | | : : : | | | :
 Db 591 EPIIDEPASFYRHD-----KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy 650 KKQYTSIHGHVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
 : | :|| | |||||: || ||||| ||:
 Db 643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683

Search completed: July 26, 2004, 12:44:43
 Job time : 12 secs